A tropical mycological journey

MON 1

Sharon A. Cantrell

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Abstract

Since starting my M.S. degree in 1989 at the University of Puerto Rico-Mayagüez, I have been involved in studying tropical fungi, and this has been a wonderful journey from the beginning. Throughout my career, I have been blessed, and I have met multiple mycologists that have impacted my life. My studies in tropical fungi have included a diversity of ecosystems from extreme to the wettest tropical forests in the Caribbean. My contributions not only include describing new species but also their ecosystem function and particularly how fungi can be affected by natural disturbances and climate change. Diversity is the theme of this year’s meeting, and I feel blessed to have served as MSA President from 2018-2019, especially being the first Latin-American to serve as President. This was a dream I had a long time ago, and throughout my life everything that I have planned has become a reality, so to all the young mycologists, never be afraid of setting the highest goals in your life because dreams come true. Life is a journey and we have to make the best of it.
Prescribed fire intervals impact soil fungal community trajectories in Florida Longleaf Pine ecosystems

MON 2

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Abstract

Prescribed fires are a management practice designed to mimic naturally occurring fire regimes and reduce fuel loads. However, it remains unclear how the soil-inhabiting fungal communities respond to frequent prescribed fires. To record fungal community responses, we utilized a 60-year fire experiment in the longleaf pine dominated Olustee Experimental Forest located in the Osceola National Forest in Northeastern Florida. The experiment includes replicated (6 replicates) stand-level fire treatments applied at 1-, 2-, and 4-year intervals in addition to unburned stands during the experiment. We sampled the A, E, and B soil horizons from all stands a week before and one month after prescribed burning stands assigned to the 1-, 2-, and 4-year burn cycles. The extracted genomic DNA was amplified with fungus specific primers (fITS7; ITS4). Congruent with other experiments, our data suggest that prescribed burn intervals maintained on decadal scales result in distinct fungal communities and that the top most soil horizons are most strongly impacted. Our work contributes to building foundational knowledge on how soil fungal communities are impacted by fires, whose intervals vary. Our data aids in choosing strategies for optimal management to maintain fungal biodiversity in soils.
Wildfire impacts on below-ground communities depend on soil horizon, site location, and burn severity: toward a framework of ecosystem recovery

MON 3

Shawn Brown\textsuperscript{1}, Allison Veach\textsuperscript{2}, Jonathan Horton\textsuperscript{3}, Ari Jumpponen\textsuperscript{4}, Richard Baird\textsuperscript{5}

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Abstract

Decades of fire suppression coupled with climatic changes have increased the frequency and severity of wildfires. The Southern Appalachia region of the United States is particularly susceptible to increased fire severity and occurrence. These fires can reorganize local biodiversity and elicit short- and long-term shifts in microbial communities, which can lead to fire adapted communities that follow novel community trajectories and facilitate ecosystem recovery in different ways. Following the record-breaking 2016 fire season in Southern Appalachia, we examined wildfire impacts on below-ground communities within two substrates (duff and soil) at two adjacent locations with similar plant communities (Great Smoky Mountains National Park – Chimney Top 2 Fire and Nantahala National Forest – Cliffside Lake Fire) from eight replicate plots representing a range of fire severities (Unburned, Low Severity, Moderate Severity, Severe). Soil-inhabiting communities differed across the fire severities. Further, fire impacts on communities and functional guilds were location- and substrate-specific: Nantahala National Forest sites were relatively more fire-sensitive than Great Smoky Mountains National Park sites and soil more fire-sensitive than duff. Ectomycorrhizal abundance did not change in duff with fire but decreased in soil with burn severity whereas putative plant pathogens increased with burn severity but did not change in soil. Despite distinct communities across fire severities, traditional fire-responsive (phoenicoid) fungi remained absent although several fire-responsive OTUs could be identified thus highlighting our poor understanding of fire responsive fungi. Taken together, our results suggest context-dependency in fungal responses to fire that must be accounted for to generate ecosystem-wide recovery predictions.
Mycorrhiza of Pine Seedlings (*Pinus pungens*) germinating after the Chimneys 2 fire in the Great Smoky Mountains National Park

MON 4

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Abstract

A wildfire in the Great Smoky Mountains National Park (November 2016) burned three ridgetop populations of the Appalachian endemic Table Mountain Pine (*Pinus pungens*). *Pinus pungens* is serotinous and by June, 2017, small pine seedlings were sprouting in these severe burn areas. Throughout 2017 and 2018, mycorrhiza on the roots of these seedlings were examined for ectomycorrhizae and, where feasible, their nrITS sequences were obtained. We show that even tiny pine seedlings formed mycorrhizae prolifically. Mycorrhizae on pine roots differed between the three high severity burn sites and changed over time. Some mycorrhizae apparently acted to bind soil, forming a sticky outer coating that was complexed with small soil particles. Predominant mycorrhizae on pine seedlings were in the Pezizaceae (including *Sphaerospora*), and the basidiomycetes *Laccaria trichodermophora* and *Thelephora* spp. Mycorrhizae shared across the three severe burn areas included *Hydnotra*, *Rhizopogon* and *Tuber*, all sequestrate fungi which may have survived the fire.
Ectomycorrhizal dynamics of whitebark pine seedlings in wildfire-impacted soil: and implications for restoration

MON 5

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Abstract

White bark pine (*Pinus albicaulis*) is an iconic, five-needle, high-elevation pine whose existence is threatened by an exotic rust, mountain pine beetles, fire suppression, and climate change. Its distribution is limited to western North America and populations have declined 90% in recent decades. The pine is shade intolerant and depends on wildfire to reset the successional clock. Regeneration occurs mainly through germination of un-retrieved seeds planted by nutcrackers on burns after wildfire. However, regeneration does not always follow wildfires or prescribed burning, and thousands of nursery seedling are being planted across the landscape to compensate losses. We examined how the ectomycorrhizal fungi (EMF) in whitebark pine forests are impacted by fire through a series of field and greenhouse studies. Field studies in Montana and Alberta found that 1) species richness of EMF was low 2) intense fire in compromised beetle-killed stands could wipe out all EMF 3) intense fire in a healthy mature forests reduced EMF species richness 40-50%, shifted EMF communities, and reduced suilloids (*Suillus, Rhizopogon*) on seedling roots five years postfire 4) EMF can survive light prescribed burns. In greenhouse and *in vitro* studies, we found that 5) various *Suillus* species access different nitrogen sources 5) in burned soil, *Suillus americanus* (*sibericus*) inoculation increased seedling biomass 61%, leaf nitrogen content 25%, and lowered δ¹⁵N. *Suillus americanus* was used to inoculate pines for several large restoration projects on burns involving thousands of nursery-generated whitebark pine seedlings in Canada and Montana; results will be discussed.
Prescribed fire reorganizes fungal communities and alters microbial decomposition in the long-leaf pine savanna of North America

MON 6

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Abstract

Frequent fires sustain pyrogenic ecosystems. In many of these systems, recurrent fires maintain a tree-grassland “matrix” and generate heterogeneous microhabitats that support high species diversity. Aboveground responses to fire in pyrogenic systems have been well-studied, but responses of belowground communities, such as fungi, remain poorly known. We assessed fire effects on fungal communities and decomposition rates in a pyrogenic pine savanna in North America. Fungal communities in litter and soil substrates were sampled in recently burned and unburned microhabitats located near or away from pines. Soil properties and vegetation composition were sampled to assess drivers of fungal communities other than fire. Fresh litter from the field was collected from unburned plots, sterilized, placed in nylon mesh bags, and deployed to the field to assess differences in microbial decomposition over time among burned and unburned areas. Fire caused substantial changes in fungal communities and strongly reduced decomposition, despite only having small effects on soils and vegetation. Fire favoured specific (pyrophilic) fungi, while reducing most saprotrophic and ectomycorrhizal taxa. Fungal community changes from fire were greater in litter than in soils. Our data suggest this pyrogenic savanna contains fire-adapted fungal communities including both fire-resistant and fire-sensitive taxa. Fire-suppression of saprotrophs resulted in reduction of fuel decomposition, which could enhance spread of future fires across the previously burned areas. Thus, reorganization of the fungal community associated with fires may enhance persistence of these fire-adapted ecosystems.
Using traits to predict fungal succession and ecosystem regeneration after wildfires

MON 7

Sydney Glassman
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Abstract

After wildfires, forest recovery depends on ectomycorrhizal fungal (EMF) spores surviving and serving as partners for regenerating forest trees. The difficulty in predicting wildfire events forces fungal ecologists to rely primarily on space-for-time comparisons, laboratory heating experiments, and prescribed burns to understand the effects of wildfires on fungi. But, stand-replacing fires are unique because of heat intensity and widespread host death.

Here, I take advantage of Mega-Fires burning two plot networks to test the response of EMF to severe natural wildfires. I originally sampled soil fungi using high throughput sequencing methods for separate plot networks of both *Pinus ponderosa* (F. Pinaceae) in 2011 and *Notholithocarpus densiflorus* (F. Fagaceae) in 2013. In 2013, the Rim Fire burned the *P. ponderosa* plots. In 2016, the Soberanes Fire burned the *N. densiflorus* plots. In both cases, I was able to re-sample the same sampling locations within weeks of the fire before the dispersal of new spores via winter rains. I sequenced the soil and assayed the EMF spore banks using greenhouse seedling bioassays. Thus, I tested which fungi survived the Mega-Fires and if there were generalizable traits amongst fungi that survived in two different forests.

For both *P. ponderosa* and *N. densiflorus* plots, fungal communities were reduced in alpha and beta-diversity after the fire, but certain groups of taxa increased in frequency after fire. In both Mega-fires, genera of truffle forming EMF increased in frequency after the fire. Thus, generalizable traits of fire adapted fungi are beginning to emerge.
Chytridiomycota: Under-explored components of marine fungal biodiversity in extreme environments

MON 8

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Abstract

The loss of sea ice is reducing albedo and allowing increased light penetration into the Arctic Ocean. Increased light is stimulating phytoplankton blooms and altering the associated heterotrophic microbial community. Recent high-throughput sequencing and 28S rRNA clone-based studies of eukaryotic microbial diversity revealed that the fungal community in Arctic sea ice is predominated by an uncharacterized clade of Chytridiomycota that branch sister to the Lobulomycetales. These Chytridiomycota parasitize ~1% of all diatoms and 25% of a single species in brine channels where salinities can exceed 100. In this system, snow cover, explained nearly half of the variability associated with the incidence of Chytridiomycota parasitism on diatoms. Novel Chytridiomycota-specific CARD-FISH probes revealed substantial Chytridiomycota throughout the Arctic Ocean. When flow-cytometer sorted-CHN quantified carbon values of cultured Chytridiomycota isolates were applied to CARD-FISH counts, biomass was found to be 11.66 mg C m\(^{-2}\) in seawater. Together, these data demonstrate that the Chytridiomycota are active members of Arctic marine ecosystems. To expand on these observations, publically available high-throughput sequencing databases were downloaded and reprocessed. In extreme environments (>10 standard deviations away from the global salinity mean), such as the Baltic Sea, Red Sea, and in sea ice, the Chytridiomycota were found to predominate the fungal community, suggesting unrealized relevance to global marine ecosystems.
Linking fungal community composition with the process of wood decay in terrestrial, freshwater and marine habitats in the tropical eastern Pacific

MON 9

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Abstract

Wood decomposition plays a critical role in the carbon cycle, and in sustaining aquatic ecosystems, however dynamics of decay processes in water are poorly understood. To explore how fungal communities, assemble and influence decay we placed Guazuma branch wood sections on land and along salinity gradients in three rivers in Panama. After 15 months, mass loss was greater on land than in freshwater, but did not differ from marine and estuarine, where up to 50% of wood was removed by shipworms. Slower decay in freshwater was associated with the retention of higher wood carbon:nitrogen ratios, and higher concentrations of cellulose, hemicellulose and two lignin moieties through the experiment. Sequencing of the ITS and LSU fungal primers revealed large habitat differences in fungal diversity and composition. The terrestrial wood-associated community was three times larger than the freshwater community, and six times larger than the marine community. Hierarchical clustering and NMDS ordination revealed that fungal communities grouped primarily by habitat, rather than census or river. For Ascomycetes, there were clear order-level distributional affinities, e.g., Jahnulales, Magnaporthales and Annulatascales dominant in freshwater, Microascales and Lulworthiales in estuarine and marine water, and Leotiomyctes, Chaetosphaeriales and Xylariales on land. For Basidiomycetes, most orders were significantly associated with terrestrial habitats, and three orders (Atheliales, Septobasidiales and Malasseziales) present in freshwater and estuarine habitats. Habitat differences in decay rate may in part reflect variation in fungal communities, which show compositional differences at the phylum and order level as well as major shifts in diversity across habitats.
Marine fungi research in the eastern South Pacific Ocean off Chile

MON 10

Marcelo Gutiérrez\textsuperscript{1,2}, Silvio Pantoja\textsuperscript{1,2}

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Abstract

While the number of studies on fungi in marine environments has significantly increased over the last few years, they remain as one of the less known functional groups of microorganisms in the ocean. In ca. 10 years of studies of marine fungi in the eastern South Pacific Ocean off Chile we have unraveled novel aspects of their distribution, diversity, biochemical composition and functions. Our early studies in the coastal upwelling ecosystem off Chile evidenced the presence of individual and dense conglomerates of fungal mycelia and spatial variability in abundance and diversity of marine fungi linked to physicochemical and biological gradients in coastal waters. At the temporal scale, our results showed both similar biomass of filamentous fungi to that of prokaryotes under active upwelling conditions and a seasonal pattern in fungal abundance associated with increases in phytoplankton biomass. We described for the first time the role of fungi in degradation of organic macromolecules in the marine ecosystem as well as the parasitic action of chytrid fungi on marine diatoms, suggesting a potential role controlling phytoplankton populations in the coastal ocean. Results on biochemical composition of culturable marine fungi have also evidenced a potential role of fungi supplying nutritious molecules to marine trophic webs, and a unique biomarker imprint with potential applications in biogeochemical studies. Our findings provide new insights into ecological and trophic interactions of marine fungi and bring support to their inclusion in models of microbial loop and carbon cycling in the ocean.
Investigating the taxonomy, diversity, and ecology of *Fusarium* species associated with marine animals

**MON 11**

Christopher Smyth¹, Jullie Sarmiento-Ramírez², Dylan Short³, Javier Diéguez-Uribeondo², David Geiser¹

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**Abstract**

*Fusarium* is a widespread genus of ascomycete fungus well known for its roles in plant disease, mycotoxin production, opportunistic human disease, as well as veterinary infections. The *Fusarium solani* species complex (FSSC) contains the *Fusarium* species most frequently associated with veterinary infections: *F. keratinophilum* (Fk), *F. falciforme* (Ff), and unnamed phylogenetic species FSSC 12. While Fk and Ff are associated with a variety of environments, all known isolates of FSSC 12 are derived from, or associated with, infections of captive marine animals. The unique association of FSSC 12 with captive marine animal infections highlights the need for a formal species description. In addition, we assessed physiological characteristics that may be important for the strong association between FSSC 12 and marine animals. While not unique to marine animals, Fk and Ff have recently been associated with mortalities in sea turtle nests worldwide, called sea turtle egg fusariosis (STEF). Little is known about the ecology and epidemiology of Fk and Ff as it relates to STEF. We conducted surveys along Florida beaches to determine the diversity of *Fusarium* species in nesting environments, as well as the association between pathogen presence and hatching success. Fk and Ff were the only FSSC species isolated from both hatched and unhatched sea turtle eggs, and *Fusarium* communities in the sand outside of nests were significantly more diverse. Our findings suggest Fk and Ff are endemic to nesting environments, and factors other than pathogen presence may play an important role in the development and severity of disease.
Generating reference sequences and distribution data for dark matter fungi in marine environments

MON 12

Kathryn Picard
National Museum of Natural History, Smithsonian Institution, Washington, DC, USA

Abstract

The quality of high throughput sequencing (HTS) platforms continues to rise as the per-base cost continues to fall, making HTS more useful and accessible than ever. However, in culture-independent surveys of fungal communities across habitats, it is not uncommon to find a significant fraction of reads that cannot be identified to any taxonomic level beyond kingdom or phylum. The increasing adoption of next-generation sequencing methods over traditional culturing surveys has ultimately reduced the rate of new sequence incorporation into reference databases. Barring a concerted effort to improve the taxonomic sampling of these reference databases, our capacity to sequence novel phylotypes will continue to outpace our ability to identify them. In this talk, I will discuss advances in long-read sequencing that allow for the generation of high-quality, multi-locus sequence data for uncultured fungi from environmental samples. Using data generated from diverse marine habitats including sediment cores, intertidal zones, and the deep sea, I will demonstrate that long reads provide improved taxonomic resolution, even overcoming the deficiencies of extant reference databases. Moreover, I will show that long-read sequences can bridge studies employing different target loci (ITS1 vs. ITS2 vs. 28S), allowing for the inference of distribution patterns that were previously unavailable.
**Diversity of the mycobiota of deep-sea sediments from the Gulf of Mexico**

**MON 13**

Lluvia Vargas Gastelum, Dolores Camacho, Meritxell Riquelme

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**Abstract**

Fungi from marine environments have been understudied in comparison with those from terrestrial environments. To study the distribution patterns of the benthic mycobiota of the Gulf of Mexico, over the course of four years (2015-2018) we have analyzed sediments collected from the Mexican Exclusive Economic Zone (EEZ), including the Sigsbee Deep basin, with depths ranging between 1000 m and >3500 m. Internal Transcribed Spacer 1 (ITS1) amplicons were sequenced by Illumina MiSeq. A total of 4,421 Operational Taxonomic Units (OTUs) were obtained, indicating a high fungal richness. Most OTUs assignments corresponded to members of the Ascomycota, unidentified fungi, and Basidiomycota. The majority of the stations shared only 31 OTUs, which included the worldwide reported genera *Penicillium*, *Rhodotorula* and *Cladosporium*. We identified the presence of both a large transient community and a conserved community, which are dependent or adapted to changes in the habitat dynamics, respectively. We found that the potential drivers delimiting fungal distribution were principally carbon content and geographical location. Some of the fungal isolates that we were able to recover from the sediment samples were identified as: *Cladosporium halotolerans*, *C. dominicanum*, *C. iranicum*, *Stemphylium* sp., *Alternaria alternata*, *Penicillium chrysogenum*, *P. corylophilum*, *Biatriospora* sp., *Hortaea thailandica*, *Curvularia* sp., *Aspergillus creber*, *A. jensenii*, and *Verrucoconiothyrium prosopidis*. This study contributes to expand our knowledge on the biogeography of the fungal community from deep-sea sediments, where the geographical and physicochemical properties delimit fungal composition and distribution.
Centimeter-scale structure and multi-year temporal persistence of arboreal fungal communities in a Costa Rican rainforest

MON 14

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Abstract

Aboveground tree canopies and branches in the tropics provide important habitats for diverse plants, arthropods and fungi. However, the fungi of these habitats have been little studied in comparison to leaf epi- and endophytes and soils. In soils, fungal communities are often patchy at meter scales. In the context of a study of epiphytic orchid mycorrhizae, we carried out a detailed analysis of the substrate preferences and spatial-temporal dynamics of total fungal communities in substrates on branch surfaces in a lower montane rainforest in Tapanti National Park, Costa Rica. We sampled 120 points from adjacent branches of the host Sauauiia montana, with pairs of samples ranging from 1 cm to ~8 m apart, separated the samples into component substrates, and carried out Illumina ITS2 sequencing. We resampled a subset of these points in the second and third years of the study. Fungal diversity was extremely high (~5500 OTUs) and many samples had no fungal species in common. Despite this high turnover, we detected moderately strong spatial autocorrelation in community composition from 1 to 50 cms. This similarity tapered off at 50 to 100 cms. Fungal communities in live bryophytes, dead bryophytes/litter, bark surface and inner bark were all distinct by perMANOVA, although many taxa were found in all four substrates. Despite the cm-scale structure, locations were more similar over two years than predicted by chance, indicating temporal persistence. While the ecologies of most of these fungi are unknown, their patchiness likely impacts orchids, which are often mycorrhizal specialists.
Endophytic *Trichoderma* with fungicide tolerance.

**MON 15**

Efrain Escudero, María del Milagro Granados, Eduardo Alvarado, Jason C. Slot, Ana P. Alonso, Priscila Chaverri

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**Abstract**

Pesticides, including fungicides, are still widely used in agriculture. For example, the majority of coffee farms in Costa Rica use them intensively, where a single fungicide (i.e., mancozeb) represents about 25% of the agrochemicals imported in the last 30 years. Therefore, an important challenge in the transition to organic agriculture is the effectiveness of biocontrol agents when pesticides and fungicides remain in the soil for many years. One strategy to transition from conventional to organic agriculture would be to use biocontrol agents that tolerate these agrochemicals. As part of a larger project to find antagonistic fungi against coffee (*Coffea arabica*, Rubiaceae) diseases, several species of endophytic *Trichoderma* have been tested against two important pathogens: *Colletotrichum cf. acutatum* and *Mycena citricolor*. The endophytes were isolated from wild Rubiaceae plants in Costa Rica. Of these, *Trichoderma rifaii*, *T. strigosellum*, *T. vires*, and *T. sp. nov.* had the strongest antagonistic effect. The objective of this study was to determine if these *Trichoderma* spp. could tolerate and grow in the presence of seven widely used fungicides in coffee production. Growth of the *Trichoderma* spp., *Colletotrichum cf. acutatum* and *Mycena citricolor* with and without fungicides was measured *in vitro*. All the fungicides showed a dramatic inhibition of both pathogens (~80%). On the other hand, six of the seven fungicides tested were almost innocuous to the endophytic *Trichoderma* spp. Results from this study suggest that these endophytic *Trichoderma* spp. should be able to colonize and prevail in coffee plants and plantations where soils are contaminated by fungicides.
Testing for adaptation: Nitrogen metabolism by fungi after long term nitrogen addition

MON 16

Nora Duncritts, Anne Pringle
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Abstract

Global change may be forcing species to adapt or face potential extinction. Human-derived nitrogen pollution and its subsequent deposition on soils is an increasing phenomenon of changing environments and potentially an immense stress on ecosystems. Whether or how organisms and species are adapting in the face of global change is an emerging focus of research, but measuring adaptation can be difficult. Fungi are critical to biogeochemical cycles, but because individuals grow hidden in substrates, fungi have been historically difficult to manipulate. The dynamics of fungal adaptation to global change remains an almost wholly unstudied phenomenon. While changes in the composition of fungal communities caused by nitrogen pollution are documented, the ability of fungi to adapt their metabolisms to nitrogen stress is unknown. I am testing the uptake and use of nitrogen by fungi which have been subjected to long term nitrogen pollution and am comparing their growth to the growth of fungi which have not been exposed to nitrogen pollution. I aim to demonstrate whether fungi experiencing nitrogen pollution have adapted to grow preferentially on nitrogen from pollution sources, which are chemically distinct from natural sources of nitrogen. By tallying a total nitrogen budget for isolates of the same species exposed or not exposed to nitrogen pollution, I am testing whether adaptation has occurred, and potentially how this will impact decomposition in contexts of global change.
Assemblage Structure of Ectomycorrhizal Fungi on *Quercus ilicifolia* (Scrub Oak) in Fire Adapted Pine Barrens: Results from Field-collected Roots and Lab Bioassays

**MON 17**

Aimée Hudon¹, Thomas Horton¹, Neil Gifford²

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**Abstract**

Ectomycorrhizal fungi (EMF) are thought to contribute to establishment of host plants after disturbance such as fire. A species rich group of EMF are found with pines in undisturbed settings. A different assemblage of EMF are found on pine seedlings after fire that occur as resistant spore banks in soils and can be observed using soil bioassays. The objective of our study is to investigate if this dynamic occurs in *Quercus ilicifolia* (scrub oak) communities. We document EMF on *Q. ilicifolia* at the Albany Pine Bush Preserve where fire is an integral part of the community. We collect *Q. ilicifolia* roots along with surrounding soil from relatively undisturbed sites. Roots are sorted into morphological types (morphotypes). Associated soil is air dried to select resistant spore inoculum and used in a laboratory bioassay with *Q. ilicifolia* seedlings in a paired design with field and bioassay data linked. Morphotypes are identified using the fungal barcode (nrITS region). ITS sequences of unique RFLP patterns are submitted to GenBank for identification. We use species richness and Simpson’s and Shannon-Weiner diversity indices to assess if there is a difference in assemblages of EMF colonizing roots from field (n=32) verses soil bioassay (n=31). We expect bioassay seedlings to be colonized by a different assemblage of EMF than offshoots harvested in situ. Results may reveal EMF in oak systems that respond to disturbances such as fire and elucidate how EMF contribute to oak recovery and restoration.
Drivers of endophyte communities of the invasive plant Kudzu (*Pueraria montana var. lobata*): toward a framework of integrated invasive plant management

**MON 18**

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**Abstract**

Plant endophytes, microbes that colonize plant tissues but are asymptomatic, are a hidden world of diversity that play an important role in plant health and fitness. Kudzu (*Pueraria montana var. lobata*) is a highly aggressive invasive that has become a dominant weed in the Southeast United States and covers almost seven million acres. Kudzu acts as a reservoir for Asian Soybean Rust (*Phakopsora pachyrhizi*) as well as many other pathogens that infect leguminous crops. Toward a goal of developing management strategy for Kudzu to reduced pathogen spillover using an integrated endophyte-pathogen framework, we drivers of Kudzu endophytic and pathogenic communities (Illumina MiSeq) across the main invasive range in the United States (TN, MS, AL, GA). Additionally, we measured multiple parameters including physicochemical (Chlorophyll, NO$_3^-$, K$^+$, soil pH), leaf trait (leaf surface area), genetic (genotype) and geographic information (region and traffic volume). Fungal communities were diverse and structured by multiple variables (in PERMANOVA analyses, but location, genotype, traffic volume (proxy for pollution), were the main drivers of endophytic communities ($R^2$=0.152, $R^2$=0.129, and $R^2$=0.126 respectively). Further, OTU richness ($S_{obs}$) and diversity ($1-D$) estimates changed across geography and with traffic volume. Taken together, these data suggesting that host-genetics and local pollution play important roles in structuring Kudzu endophytes and integrative plant management must consider these factors when developing management strategies.
ORGANIC MATTER REMOVAL IMPACTS FOREST FUNGAL COMMUNITY AND TREE PHYSIOLOGY

MON 19

François Maillard¹, Elisa Thebault², Valentin Leduc¹, Chloé Viotti¹, Cyrille Bach¹, Emmanuelle Forin¹, Lucas Auer¹, Dominique Gérant³, Marc Buée¹

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Abstract

Growing demand for renewable energy and materials has led to intensified forest management practices and harvest activities. Combining forest soil fertility and soil carbon storage with the intensification of forest practices represents a major challenge. While microbes assume a key role in carbon and nutrients cycle in the forest, the impacts of greater forest management activity on fungal community remains poorly studied. To tackle this question, we based our study on a large scale organic matter manipulation experimental network mimicking intensive forestry practices. We investigated the effects of organic matter removal on soil properties, tree growth, total fungal composition and functioning as well as targeted analyses of associated ectomycorrhizal fungi. In comparison to conventional practices, we highlighted a decrease of nutrient mobilization functions by fungi and a switch from plant-derived to microbe-derived organic matter as a fungal nutrition source. We found a strong restructuring of the fungal community toward yeasts and ectomycorrhizal fungi in response to organic matter removal. We showed that amino acid content of ectomycorrhizal fine roots drastically decreased with a concomitant increase of hexose content, which we speculate was caused by insufficient nutrient transfer between ectomycorrhizal fungi and their associated tree hosts. Collectively, these results reveal that soil fungi are early and sensitive indicators of forest disturbance. We suggest that while intensive forestry could represent a threat for forest soil fertility it may not impede soil carbon storage due to positive impacts on specific fungal guilds slowing the decomposition of organic matter.
Tallgrass prairie soil microbial communities across two alternate states: how do fungi respond to fire and woody encroachment?

MON 20

Laura Mino, Ari Jumpponen, Lydia Zeglin
Kansas State University, Manhattan, USA

Abstract

Widely considered to be one of the most perilously threatened ecosystems across the globe, grasslands continue to be threatened by a variety of global change phenomena and anthropogenic influences. Current estimates state that, after decades of conversion to row-crop agriculture, as little as 1% of the historic range of the North American tallgrass prairie remains intact. The remaining prairie continues to be threatened by woody species encroachment, wherein land management choices including the suppression of fire facilitate a transition from grassland to shrub- and/or woodland, resulting in a shift to an alternate ecosystem state. The woody-encroached state affects ecosystem productivity and biodiversity, renders pastureland less suitable for grazing, and alters key ecosystem functions above and below ground. Frequent, recurring fire attracts the non-encroached grassland state, but restoration of woody-encroached states using fire have found little success. Soil fungi are critical in determining plant community structure; however, little research exists on potential differences between soil microbial communities associated with these alternate states, or how these communities may differentially respond to re-introduced fire regimes. To improve our understanding of soil microbial community composition and dynamics in response to fire, we dissected fungal and bacterial communities before and after fire in both encroached and non-encroached states and describe soil microbial responses on a high temporal resolution scale. We characterize fungal and bacterial abundance and community composition using qPCR and Illumina MiSeq (16S and ITS). Understanding compositional and functional responses of these communities to fire likely offers insights into conservation of remaining grasslands and restoration of encroached woodlands.
Fruiting response of ectomycorrhizal fungi to nutrient additions in Bartlett Experimental Forest, New Hampshire

MON 21

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Abstract

Ectomycorrhizal fungi (EMF) form mutualistic symbioses with a variety of tree species and fill many functional niches in forest ecosystems. EMF improve nutrient and water accessibility for plants, reduce root herbivory, and protect against soil pathogens. Therefore, a change in a forest’s fungal composition may impact trees in diverse ways. The community composition of EMF in forest soils may be sensitive to changes in the nutrient environment in ways not yet fully described. Our research investigates ectomycorrhizal community responses to nutrient manipulation in a project on Multiple Element Limitation in Northern Hardwood Ecosystems (MELNHE) in which nitrogen (N) and phosphorus (P) have been added in a full factorial design since 2011. Mycorrhizal sporocarps were collected five times from July – October 2018, identified by morphology, and quantified in six stands across two successional stages: mid-aged (clear-cut between 1970-1979) and mature (clear-cut between 1880-1890). Morphological types (morphospecies) were analyzed using ANOVA and modeled using multivariate community ordination. Sporocarp abundance and morphospecies richness responded to N and P additions differing by forest successional stage. Community composition described by ordination differed by treatment and throughout the season. Morphospecies identities will be confirmed using the fungal barcode (ITS region) and all analyses will be repeated. While mycorrhizal fungi are known to respond to N fertilization, this work is among the first to observe sporocarp response to P fertilization, and N and P fertilization together, which will be important to predicting how fungal communities will respond to changing soil conditions in a changing world.
Plants as substrates: the evolutionary origins of epiphytism in lichens

MON 22

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Abstract

Lichens occupy a diverse range of substrates, including rock, tree bark, and leaves. Epiphytic lichens play important roles in precipitation interception, nutrient-cycling, and as food and habitat for diverse animals. While epiphytic lichens may experience reduced competition for substrate space with vascular plants, they also face physiological challenges such as increased desiccation. Here we ask: when did lichen-forming fungi invade arboreal habitats, and what were the macroevolutionary consequences of this transition? We focus our efforts on the class Lecanoromycetes, the most diverse clade of lichen-forming fungi, and address these questions by performing ancestral state reconstruction on a time-scaled phylogeny of the class. We then discuss the paleoecological implications of these transitions, and place them in a broader and more comparative framework by discussing them in the context of climate, vegetation, and the evolution of other epiphytic or arboreal lineages.
The genus *Cladosterigma*: a mycological enigma finally revealed.

**MON 23**

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**Abstract**

*Cladosterigma clavariellum* has been treated as a basidiomycete since its original description by Spegazzini in 1886 as *Microcera clavariella*. After a series of reviews between 1919 and 2011 it remained allocated among the basidiomycetes, lately as a genus *insertae sedis* in order Cryptobasidiales. Our studies, based on light and scanning-electron microscopy, supported by solid multilocus philogenetic analyses, finally determined the true nature and phylogenetic position of the genus *Clavariella* as the first mycoparasitic member of a new family (*Cladosterigmaceae*) within Graphidales, (Ostropomycetidae, Lecanoromycetes), an order previously accommodating exclusively lichen-forming fungi.
Fungal pathogens associated with cultivated rubber trees in Sri Lanka

MON 24

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Abstract

Fungal pathogens are regarded as one of the major threats on rubber trees worldwide. Although rubber pathogens are traditionally known based on morphology, less or no molecular data are available for some pathogenic species in Sri Lanka. Emergence of new pathogens due to climatic changes and introduction of new clones is a probable event. Therefore, assessment of fungal pathogens associated with rubber trees in Sri Lanka is imperative. The major objective of this study is to accurately identify foliar fungal pathogens associated with rubber plants in Sri Lanka using morphology and phylogenetic analysis. Single spore isolation was carried out to obtain pure cultures of fungi from diseased leaf samples collected randomly from selected sites. Internal transcribed spacer loci of all isolates were sequenced along with Glyceraldehyde-3-phosphate dehydrogenase for some isolates. Phylogenetic analysis was performed to confirm the relative phylogenetic placement of species. According to the morphological and molecular data, Curvularia verruculosa, Colletotrichum truncatum and Colletotrichum gigaasporum complex species identified in this study were the first global host association records on rubber. Three isolates were first records of host-pathogen association locally; Colletotrichum siamense, Curvularia senegalensis and Phyllosticta capitalensis. Both of the Curvularia spp. recorded are first records of the fungus in Sri Lanka. Pathogenicity tests conducted for Colletotrichum isolates proposed, typical anthracnose symptoms are correlated with the gloeosporioides complex species while C. gigaasporium and C. truncatum species are capable of successfully colonizing on rubber leaves. Hence, this study reveals the unknown diversity of foliar fungi associated with cultivated rubber trees.
Phylogenetic resolution of entomophthoralean fungi that infect cicadas including a new genus that infects scrub cicadas (Diceroprocta spp.)

MON 25

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Abstract

The Entomophthorales (Zoopagomycota) are among the earliest diverging and most significant arthropod-destroying fungi. Yet, these entomopathogens remain vastly understudied due in part to their ephemeral obligate lifestyle, a paucity of specimens in natural history collections, and sub-optimal storage of many specimens that do exist. One genus, Massospora, which contains more than a dozen obligate, sexually transmissible pathogenic species that infect cicadas (Hemiptera) worldwide, has recently gained significant attention following the discovery of psychoactive alkaloids from two behavior-modifying species. Additionally, the discovery that M. levispora and M. platypediae seemingly comprise a single annual-cicada infecting Massospora species that occupies a broader geographic and host range than previously reported, raises questions about the phylogenetic relationships among other cicada-infecting “Massospora”. The recent acquisition of archived M. diceroproctae-infected scrub cicadas (Diceroprocta semicincta) as well as M. tettigatis from several species of Tettigades cicadas across Chile provided an opportunity to conduct a phylogenetic analysis to determine if these cicada-infecting fungi are monophyletic. Here we report that “Massospora” infecting Diceroprocta semicincta, although a member of the Entomophthorales, forms a distinct clade separate from the monophyletic clade that contains M. cicadina, M. levispora, M. platypediae, and M. tettigatis based on LSU DNA sequences and represents an independent occurrence of active host transmission behavior by an Entomophthoralean fungus. These results coupled with divergent spore types in M. dorisiana and M. carinetae further emphasizes both opportunity and need for a comprehensive approach to study Massospora and other unculturable Entomophthorales.
Systematic analysis of *Russula* in the North American Rocky Mountain alpine zone

**MON 26**

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**Abstract**

*Russula* Pers. (Russulales, Russulaceae) is an important ectomycorrhizal genus in alpine and Arctic regions where it is found in association with *Salix*, *Betula*, *Dryas*, and *Polygonum*. Despite *Russula*’s importance and abundance in alpine systems no research has performed an in-depth analysis of the genus in the Rocky Mountain alpine. Seven species of *Russula* were thought to be present in the Rocky Mountain alpine zone. However, these species have not been verified using molecular techniques which is necessary because the genus *Russula* is large, diverse, and intraspecific morphological variation makes taxonomic classification difficult. This research is comparing Rocky Mountain alpine *Russula* collections to Arctic and alpine collections from Europe using an in-depth morphological study and a systematic molecular analysis of the nuclear ribosomal ITS1-5.8S-ITS2 region (ITS barcode) and the second largest subunit of the RNA polymerase II gene (RPB2). Over 160 *Russula* collections have been sequenced including type and reference material. Preliminary systematic analysis has vastly increased the estimated number of *Russula* thought to occur in the Rocky Mountain alpine to at least 11 species representing multiple infrageneric classifications. This work has increased the current distribution of alpine *Russula* species throughout the world and has the potential to discover new species. A key to the identification of Alpine *Russula* in North America is provided which will promote future ecological research into the impact of this important ectomycorrhizal genus because little is known about the species present or how to identify them.
Hidden diversity of *Clavulina* (Cantharellales, Basidiomycota) in tropical and temperate Mexico: a comprehensive synthesis

**MON 28**

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**Abstract**

In the last 15 years, 19 new species of *Clavulina* have been described from neotropical ecosystems from Guyana and Brazil. These species expanded the concept of basidiome form in the genus, which was regarded to be clavarioid only. In temperate ecosystems, this genus has been considered as relatively species poor, however, our data have revealed a hidden and undescribed richness of *Clavulina* in Mexican temperate and tropical forests. This year we described nine new species for the genus from Mexico, which differ from the South American species in their relatively homogeneous clavarioid forms, and some of which resemble previously described species from Europe. Here, we synthesize the knowledge on the diversity and ecology of the genus, including molecular systematics, morphological taxonomy, community ecology, and stable isotopes analyses. The new species included are *Clavulina arboreoparva*, *C. flavopusillis*, *C. mahiscolorata*, *C. oreomunensis*, *C. parvispora*, *C. sphaeropedunculata*, *C. stipestrigosa*, *C. subtilis*, and *C. tuxtlazana*. Furthermore, we present the description of another new species (*Clavulina* sp. nov. 1) included in the “cristata complex”, collected from Mexican subtropical forests. Our results highlight the ecological relevance and taxonomic richness of this ectomycorrhizal genus, which is likely more diverse in North America than previously thought.
Diversity of agarics (dark spored mushrooms) of Punjab, India

Mon 29

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Abstract

As a result of the fungal forays conducted between 2008-2012 a total of 185 dark spored mushroom collections were made which were worked out for their morphological, anatomical and chemical reaction details. A total of 95 species belonging to 14 genera in 04 families of order Agaricales collected from different localities and sub-localities of Punjab state. Out of the identified taxa, 09 species viz. Agaricus punjabensis sp. nov., A. stellatus-cticus sp. nov., A. patialensis sp. nov., Agrocybe coprinella sp. nov., Coprinus punjabensis sp. nov., Panaeolus atrii sp. nov., Psathyrella aurantiacoumbonata sp. nov., P. plicatilis sp. nov. and P. patialensis sp. nov. are proposed as new to science proposed as new to science and 09 new varieties have been proposed, one new combination is proposed and 39 taxa have been reported for the first time from India. 11 taxa were new record for North India. Out of the total species, 11 species which are already reported from other regions of India have been recorded for the first time from Punjab state. The remaining were re-records for the area.
Rising From the Ashes: Succession and Metabolism of Post-Fire Fungi

MON 30

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Abstract

Fire transforms soil organic carbon into complex pyrolyzed carbon, which alters its accessibility for soil dwelling organisms. After a fire disturbance, soil fungi consume soil carbon and are an integral part of ecosystem re-establishment. While decades of research has defined the dynamics of post-fire plant succession, post-fire fungal succession has only recently been examined. Serendipitously, in 2013 the Rim Fire burned two long-term sampling plots near Yosemite National Park (YNP). Soil community sequencing for one year post-fire demonstrated a clear pattern of fungal succession. In an ongoing study at the Blodgett Forest Research Station (~70 miles north of YNP), we aim to confirm whether or not the fungal succession pattern observed after the Rim Fire is predictable and reproducible across a gradient of controlled fire severities. Within two months after the Rim Fire, the Ascomycete Pyronema omphalodes dominated. The Ascomycete Morchella spp. dominated four months post-fire, and then the Basidiomycete Pholiota molesta dominated ten months post-fire. These three pyrophilous fungi are capable of utilizing a broad diversity of carbon sources for growth, but each fungus occupies a unique nutrient niche that is minimally shared with the other fungi. Furthermore, these fungi respond uniquely to various chemical aspects of pyrolyzed soil. Using LC-MS/MS we tracked specific chemical shifts in soil, first as a result of fire, and then after incubation with fungal isolates. Together, these data determine the fate of pyrolyzed carbon, and demonstrate how fire-adapted fungi survive, thrive, and promote the re-establishment of forest ecosystems after wild fires.
A Novel *Xylaria* sp. is Capable of Infecting Soybean Roots and Producing Systemic Secondary Metabolites Responsible for Foliar Symptoms

**MON 31**

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**Abstract**

An emerging disease of soybean, taproot decline (TRD), has been associated with a species of *Xylaria*. Symptoms of TRD include necrosis on the tap and lateral roots with yellowing, followed by necrosis and desiccation of foliage. Elucidating the origin and etiology of this pathogen is relevant for the development of effective management practices. Initial phylogenetic analyses of DNA sequences obtained from representative isolates of TRD-associated *Xylaria* sp. suggest these isolates represent a new species in the *Xylaria arbuscula* aggregate. Incorporating U.S. herbarium specimens, determined to be *X. arbuscula* based on morphological features, showed that the origin of the TRD-associated *Xylaria* sp. might represent a change in lifestyle from saprophyte to pathogen. Foliar symptoms of TRD are quite similar to another soybean disease, sudden death syndrome, which results from the translocation of phytotoxic compounds from roots to leaves. We designed an experiment to determine whether symptoms observed on soybean foliage are produced by systemic secondary metabolites produced by the fungus in the roots. Soybean cuttings were challenged with cell-free culture filtrates. Results showed detrimental effects of filtrates obtained from the TRD-associated *Xylaria* sp. on leaves and reduced root growth. Our results suggest that symptoms observed in leaves result from the translocation of phytotoxins from roots to the leaves; however, additional work is ongoing to test this hypothesis. The protocol we have developed may provide plant breeders with the means to quickly screen soybean cultivars for resistance against TRD. Resistant cultivars will provide producers in affected areas with a TRD management option.
Transport of mineral cations by *Fusarium chlamydosporum* in a mineral doped micromodel system

**MON 32**

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**Abstract**

Fungal communities tolerate drought and low nutrient environments by accessing resources through extended and exploratory mycelial networks. Fungal mycelia food webs that can weather soil minerals remain poorly investigated, even though they significantly contribute to the nutrient uptake and cycling processes in bulk soil. We have developed micromodels doped with minerals to emulate the mineralogy of a soil environment. These micromodels serve as a platform to study nutrient transport by mycelial networks under different environmental conditions. In this work, we used the micromodels to illustrate mineral element uptake and transport by *Fusarium cf. chlamydosporum* under low nutrient and drought conditions. We observed greater hyphal density and fungal thigmotropism around obstacles and through small pore spaces (~12 µm) in mineral doped microfluidic channels. Secondary ion mass spectrometry analysis showed translocation of potassium and sodium ions within fungal hyphae grown in the mineral doped channels. In contrast, mycelia in undoped microfluidic channels exhibited lower hyphal density, no thigmotropic behavior, and no mineral cation translocation. Mineral nutrient transport by fungal hyphae bypasses competition in a resource limited soil ecosystem and gives fungi survival advantage over several other organisms. This study provides the first direct proof of hyphal translocation of mineral elements from a mineral surface under nutrient limiting conditions. Together, our findings support the existing knowledge of fungal weathering of soil minerals, while facilitating the study of signaling pathways that enables fungal sensing of mineral nutrients.
Determination for Feasible Production of Xanthone from Isolated Endophytic Fungi of *Garcinia mangostana* L. in the Philippines

**MON 33**

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**Abstract**

*Garcinia mangostana* L. had been greatly reviewed for its biological potential activity, possessing a medically essential polyphenolic compound xanthone. However, *G. mangostana* takes 10 years to fully mature before it could bear seasonal fruits that are only available during the months of July-September. Analysis on the association of the endophytic fungi which can be an alternative source of novel medicinal compound within the species is very limited. Isolation of endophytic fungi is the basal key to further study the secondary metabolite secreted by the host organism. This study provides the first morphological and molecular identification of endophytic fungi from *G. mangostana* in the Philippines and the inter-relationship between these two species in the production of xanthone. Characterization of endophytic fungi was performed using the conserved Internal Transcribed Spacer (ITS) region of the cultured samples. Between the twenty-one identified samples, the leaves of the plant appeared to be the highest inhabitation site. Identified endophytes include, *Aspergillus* sp, *Neopestalotiopsis* sp., *Pseudopythomyces* sp., *Psuedopestalotiopsis* sp., *Phaeosphaeria* sp., *Lasiodiplodia* sp., *Diaporthe* sp., and *Guignardia* sp. Eight genera were mass cultivated in malt extract broth, extracted secondary metabolites and performed High Performance Liquid Chromatography (HPLC) analyses with 254nm absorbance. Results showed, all identified endophytic fungi have the same retention time (6.492-6.502) in accordance to the standard xanthone. In conclusion, *G. mangostana* L. possesses a vast number of endophytic fungi that has a potential to become the new source of medicinal secondary metabolites.
Prediction and identification of secondary metabolism production in the cosmopolitan gut-associated zygomycete *Basidiobolus* (Basidiobolaceae, Zoopagomycota)

**MON 34**

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**Abstract**

Secondary metabolism (SM) is responsible for the biosynthesis of biologically and medically important compounds with roles in antibiosis, toxicity, plant virulence, and response to environmental cues. In the fungal kingdom, SM is best characterized within Dikarya, where ascomycete fungi are well known producers of alkaloids, peptides, polyketides and terpenes. Conversely, the prevailing hypothesis is that zygomycete fungi do not produce a comparable diversity of secondary metabolites. We present computational, evolutionary, and functional predictions of SM across zygomycete fungi, and demonstrate that while most species of zygomycetes are relatively depauperate in SM diversity, individual species of zygomycetes can be uniquely diverse in SM. We present a detailed phylogenomic analysis of SM of *Basidiobolus*, a cosmopolitan genus of Zoopagomycota associated with insectivorous amphibians and reptiles. Using computational approaches, we predicted 44 gene clusters associated with SM production. These predictions show an expansion on SM compounds synthesized by non-ribosomal peptide synthases (NRPS). These NRPSs are members of clades with genes known to produce siderophores and cyclic depsipeptides, and were most likely acquired through horizontal transfer from bacteria. These genes are expressed at levels comparable to core housekeeping genes associated with primary metabolism and initial liquid chromatography mass spectrometry data confirm the presence of multiple peptides consistent with functional NRPS biosynthetic gene clusters.
Chemical ecology of the invasive Death Cap mushroom

MON 35

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Abstract

The death cap mushroom, *Amanita phalloides*, causes more human deaths than any other mushroom. Native only to Europe, the death cap was transported across the world via potted seedlings, and now thrives as an invasive species forming mycorrhizal associations with trees in both plantations and native forests.

*Amanita phalloides* possesses two families of cyclic ribosomally-manufactured toxins: phallotoxins, which bind to actin and actin-like proteins as well as amatoxins, which inhibit RNA polymerase II. Though its effects on humans are well documented, the potential role of these toxins in the invasion success of this species success remains unknown.

Here, we explore the “novel weapons” hypothesis, the idea that invading species possess biochemical weapons novel to their invaded environment, which may confer a selective advantage over native species. We use liquid chromatography-mass spectroscopy (LC-MS) to quantify amounts of the major phallotoxins and amatoxins in *A. phalloides* in Pt Reyes National Seashore, California. We have quantified toxin amounts within a mushroom, across the main compartments of volva, stipe, and cap. We have also measured toxin variation within a site, between sites, and across several years. These values are then compared to published values of mushrooms in its native European range, to assess whether the mushroom has altered toxin levels in response to its range expansion. Lastly, the potential of these toxins in impacting native microbial and insect diversity is explored.
Cold-Adapted Denitrifying Fungi Isolated from Soil and Woodchips

MON 36

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Abstract

Some fungi can perform denitrification, a microbial respiration in which nitrate is reduced to gaseous end products such as N₂O and N₂. Denitrification process has been used to remove nitrate contamination; however, most research has been focusing on bacterial denitrification. Fungal denitrification can be useful for nitrate removal in agricultural systems because they might be able to grow at cold temperature and degrade woodchips for use as their carbon source. However, the ecology and physiology of denitrifying fungi (DF) is largely unknown. In this study, we isolated and characterized DF strains for future bioremediation purpose. DF were isolated from soil and woodchip samples by using four different media. DF were incubated at 15 and 5°C at anoxic condition. To identify the end products of denitrification (N₂O or N₂), DF strains were incubated with ¹⁵N-labeled nitrate, and gas samples were analyzed by gas chromatography-mass spectrometry (GC-MS). Strains that reduced NO₃ to N₂O or N₂ were identified using PCR and sequencing the fungal ITS region. A total of 165 fungal strains (125 and 40 strains from soil and woodchip samples, respectively) were isolated. Among those, 47 strains were identified as DF and many of them belonged to the genera Fusarium, Mortierella, Cylindrocarpon. Thirty-seven DF strains could perform denitrification at 5°C, suggesting that they may play an important role in nitrate removal at cold conditions. Notably, seven DF strains reduced nitrate to N₂ gas. To our knowledge, this is the first report of DF strains reducing nitrate to N₂ gas.
A short history of food mycology

MON 37

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Abstract

The descriptor “food mycology” was first used to describe food manufacture with the aid of fungi by the US microbiologist Dr Larry Beuchat in 1985, with the publication of his book “Food and Beverage Mycology”. The term “food mycology” has survived, but over time has become used for the study of the role of fungi in food spoilage and the health of human and animals. Food mycology as we now know it was borne out of the intersection of several existing disciplines: food microbiology – the use of Petri dishes, selective media and dilution counting; seed pathology, which provided direct plating; fungal taxonomy, essential for naming and classifying foodborne fungi; plant pathology as some food spoilage fungi are preharvest pathogens of fruits and vegetables; the fundamental study of water relations, as many foodborne fungi grow under low water activity conditions; and organic chemistry, essential for the study of secondary metabolites, many of which are now known to be toxic and are known as mycotoxins. International collaboration commenced with the organisation of a meeting called “Standardisation of Methods for the Mycological Examination of Foods” in Boston in 1984. After a second workshop in Baarn, Netherlands, in 1990, the organisation morphed into the International Commission for Food Mycology, which is still today actively promoting food mycology research. This paper will describe some of the milestones that occurred along the way, and some of the people who were instrumental in the development of food mycology as a discipline in its own right.
The Sourdough Bread Microbiome: Distribution and Function of Countertop Microbial Ecosystems

MON 38

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Abstract

Sourdough bread has fermented in kitchens globally throughout human history. However, geographic variation in sourdough starter microbial diversity and drivers of this diversity are unknown as our understanding of sourdough microecology is mostly limited to studies of industrial fermentations in Europe. In the largest ever sampling of its kind, 560 starters and background information about fermentation practices were collected from 17 countries, with heavy sampling of North America. Using amplicon sequencing of the 16S rRNA gene (bacteria) and internal transcribed spacer (fungi) amplicon sequencing, we detected 8 yeast and 11 bacterial OTUs occurring at greater than one percent abundance across samples. Samples were dominated by morphologically diverse strains of \textit{Saccharomyces cerevisiae} as well as \textit{Kazachstania spp.}, \textit{Wickerhamomyces anomalus} and many non-yeast fungi. The microbial composition of sourdough starters was poorly explained by fermentation practices or by geography. However, strong patterns of yeast/bacteria co-occurrence emerged under probabilistic analyses and hierarchical clustering revealed 17 sourdough “types” based on microbial community structure. To test if microbial taxonomic diversity correlates with sourdough functional diversity, eight of these starter “types” were analyzed for the important traits of aroma and rise by analyzing the volatile organic compounds released during fermentation and conducting sensory analysis by an expert sensory panel, and measuring dough rise using time-lapse video. In this relatively simple and ubiquitous ecosystem, we are able to explore broad questions in microecology—including patterns and drivers of microbial community structure.
Substrate Recipes Using CBD Hemp Waste for Mushroom Cultivation

MON 39

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Abstract

CBD hemp cultivation is now a very significant industry in North Carolina following its legalization. However, only the flowers of the plant are used for most commercial products, thus the industry generates a significant level of waste in the form of all other parts of the plant not used for CBD products. Mushroom cultivation has the potential of eliminating waste streams, such as the CBD hemp waste, by using the plant matter as a substrate for the mycelial stage of growth in mushroom cultivation. Growing mushrooms on pure hemp material has not always proven to be highly productive. In this study, we formulated five different substrate recipes using hemp material as a dominant ingredient to find the recipe that produced the highest growth rates. We cultivated the following gourmet and medicinal fungi species on the various substrate formulations: *Pleurotus ostreatus*, *Pholiota adiposa*, and *Ganderma lucidum*. Growth rates and mushroom production rates were measured over a period of four weeks. The highest rate of growth was observed with *Pleurotus ostreatus* on 50% cocoa coir and 50% hemp material. The lowest rate of growth was observed with *Pholiota adiposa* on 100% hemp material. The highest rate of mushroom production was also measured with *Pleurotus ostreatus* on 50% cocoa coir and 50% hemp material. The lowest rate of mushroom production was also measured on *Pholiota adiposa* on 100% hemp material.
Chopping up lettuce: changing fungal communities in response to management treatments, and implications for human health

MON 40

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Abstract

Many outbreaks of human pathogenic bacteria, such as *E. coli*, are associated with Romaine lettuce. Because lettuce leaves are consumed raw rather than cooked, the phylloplane microbes (fungal and bacterial) are often ingested by the consumer. Despite this, our knowledge about natural bacterial and fungal species associated with the phylloplane of Romaine lettuce is very limited, and yet this knowledge is necessary for understanding how this naturally occurring flora interacts with introduced human pathogens. During this project, we bought 63 Romaine lettuce heads in grocery stores in Illinois, Indiana, Ohio, and Virginia. We plated homogenized samples and isolated individual cultures using axenic techniques. These cultures were DNA barcoded with the internal transcribed spacer (ITS) region of the ribosomal DNA using Sanger sequencing. We isolated 330 cultures and generated ITS sequences for 242 of those, representing 63 unique species of fungi on the lettuce phylloplane. Of these, 9 are undescribed species in diverse genera. Interestingly, the most commonly encountered species in our Romaine lettuce cultures was an undescribed red yeast. Next-generation sequencing was conducted on the same lettuce homogenates, resulting in 630 operational taxonomic units. We compared abundances at different taxonomic levels between treatments. The fungal abundance at all levels was highest in organic lettuces, closely followed by non-organic lettuces. Comparatively, fungal abundance in hydroponic samples was almost non-existent. Our results indicate that certain groups of fungi, like yeasts, in organic samples are replaced by other groups, such as molds, in non-organic samples, likely in response to differing management regimes.
Succession of the airborne fungal community in a newly constructed cheese aging environment

MON 41

Megan Biango-Daniels, Benjamin Wolfe

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Abstract

Surface-ripened cheeses are simple microbiomes—bacteria, yeast, and filamentous fungi—that form in cheese aging facilities around the world. The molds that grow in the rinds of these cheeses are celebrated for their role in shaping their flavors, aromas, and aesthetics. Natural rind cheeses have ‘wild’ rinds (not inoculated with fungal starter cultures) and rely on fungi introduced from the environment or raw ingredients. Despite the importance of wild molds in cheese production, the ecological processes that determine fungal community development have yet to be identified. To understand how fungal communities develop in aging facilities, we partnered with a small U.S. cheesemaker in the fall of 2018. We began a long-term monitoring project using settle plates to isolate culturable fungi that colonize cheese. We sampled the airborne fungi from post-construction through the addition of cheese. Early sampling, before aging occurred, indicated variable fungi species—both in composition and abundance. After cheese was added to the facility, cheese-associated fungi increased and, eventually, outnumbered the indoor air species—with *Penicillium* spp. becoming most prevalent. Interestingly, after the addition of cheese, white phenotypes of *Penicillium* became more common—suggesting a potential phenotypic switch (blue-white transition), or an increase in abundance of white species or strains. This ongoing project will provide key insights into the development of fungal communities and more opportunities to monitor the real-time domestication of wild molds, in cheese production environments.
The feasibility of utilizing coconut husk and copra cake as substrates for oyster mushroom (Pleurotus sajor-caju) cultivation

MON 42

Vincent Enriquez

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Abstract

Marshall Islands is a coconut producing country of the Pacific Region with an abundant source of coconut husk and copra cake that are commonly used by farmers for soil amendment. The study aims to explore the potential alternative use of coconut husk and copra cake for mushroom cultivation. Mycelial growth, fruiting body, cap diameter and biological efficiency conversion (BEC) of Pleurotus sajor-caju (PSC) were evaluated to determine the most suitable coconut husk-copra cake ratio combination. Ten grams of PSC were grown separately on a 600g substrate and incubated at 28°C for 35 days. The substrates used for this study were composed of shredded coconut husk (73-98%), dolomitic lime (1%), brown sugar (1%) and copra cake (0%, 5%, 10%, 15%, 20%, 25%) with moisture content at field capacity. Treatments were distributed in 10 replications and data gathered were analyzed using DMRT (p<.05). Results revealed the following patterns: mycelial growth and BEC (10%> 15%>5%, >20% >25%>0%), number of fruiting body and cap diameter (10%>5%>15%>20%>25=0%) Thin and slowest mycelial growth occurred at 0% and 25%. No significant difference was observed among treatments 0%, 20%, 25% and between 5% and 15% of copra cake supplementation. The overall growth performance was observed to be feasible at 10% copra cake supplementation (BEC=58.4%). Results suggest that coconut husk supplemented with the right amount of copra cake could be utilized effectively as locally available alternative substrates for mushroom cultivation. This work is supported by Hatch Program (accession number: 1010361) from the USDA National Institute of Food and Agriculture
Reproduction and Dispersion of the citrus pathogen *Phyllosticta citricarpa* in Florida

**MON 43**

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*Florida Department of Agriculture and Consumer Services, Gainesville, FL, USA*

**Abstract**

Citrus Black Spot (CBS) is a disease caused by *Phyllosticta citricarpa* (Botryosphaerales, Dothideomycetes) and currently affects citrus groves in five counties in southwest Florida (Charlotte, Collier, Hendry, Lee and Polk). This disease has a unique cycle in Florida as the fungus cannot reproduce sexually due to the presence of only one mating type (MAT1-2), but rather reproduces exclusively via asexual sporulation, which confers limited dispersal ability. Here we present a novel qPCR assay to distinguish both mating types (MAT1-1 and MAT1-2) and to monitor for the possible introduction of the MAT1-1 mating type. During 2017-2019, we surveyed fruit lesions, asymptomatic leaves from tree canopy and leaf litter from previously known and newly detected CBS-positive trees, and from asymptomatic trees adjacent to CBS-positive trees. To date, we have detected only the MAT1-2 mating type in Florida, after surveying more than 850 citrus fruit lesions and 205 asymptomatic canopy and leaf litter samples from 30 groves. Our findings confirm the low dispersal ability of the asexual state of *P. citricarpa* in Florida.
Antifungal effects of leaf Extracts of three Plant Species against Colletotrichum musae the Causal agent of Anthracnose Postharvest Disease of Banana fruit

MON 44

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Abstract

Anthracnose is a postharvest disease of banana caused by the fungus Colletotrichum musae that results in major economic losses during transportation and storage. For the management of banana anthracnose, antifungal effects of three medicinal plants (Azadirachta indica, Calotropis procera and Anacardium occidentale) were assessed in this study. The extracts of the plants were prepared using water, the phytochemical constituents were determined and agar well diffusion method was used to assess the toxicity of each extract at 50mg/mL, 100mg/mL and 150mg/mL. The pathogen was isolated from banana infected with anthracnose disease. The results revealed the presence of one or more phytochemicals in each of the plant extracts. Among these were alkaloids, saponnin, tannins, anthocyannin, phenol and flavonoids. All the extracts inhibited mycelia growth of Colletotrichum musae. The inhibition of mycelia growth of the pathogen increased with increase in concentration and days of incubation. At the end of day 5 of incubation, the inhibition at 150mg/mL of all the extracts was significantly different (P<0.05) from other concentrations. However, in all, C. procera extracts gave the highest percentage growth inhibition of the pathogen at all levels of concentrations tested while A. indica extracts though effective was the least but not significantly different from A. occidentale. Therefore, since these plants are cheap, easy to obtain and extract with a simple process of maceration or infusion, more trials on the dosage and formulation on the control of banana anthracnose disease are recommended.
Population genetics of endophytic *Alternaria*

**MON 45**

**Mara DeMers, Georgiana May**

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**Abstract**

Prairie is one of the most endangered habitats in North America, with fragmentation into scattered remnant patches posing significant challenges to plants and their symbionts' response to climate change. Endophytic fungi, living asymptomatically in plant tissues, may provide an extra-genomic avenue for plants to adapt, but endophytes will not be useful to restoration managers until we better understand the adaptive and dispersal potential of these fungi. The goal of this research was to estimate the structure of genetic variation of *Alternaria* spp. living endophytically in a prairie legume host (*Dalea purpurea*). Diverse and potentially undescribed species of *Alternaria* are frequently cultured in high abundance from plants as endophytes, but standard single-locus ITS barcoding cannot differentiate among species in this genus. We used Genotyping-by-Sequencing to delimit species and characterize population structure within *Alternaria* isolated from *D. purpurea* in 15 sites spanning the 500km temperature and precipitation gradient represented by Minnesota prairies. Our results will provide insight into the dispersal patterns and standing genetic variation of endophytic *Alternaria*, information essential to predicting whether endophytes can move or adapt to climate change in highly fragmented and vulnerable habitats such as prairies. If endophytes are strongly dispersal limited or maintain low levels of genetic variation, restoration efforts may have to incorporate fungus-specific initiatives in order to preserve the diversity of these threatened ecosystems.
Environmental filtering structures diverse fungal endophyte communities in tree bark

MON 46

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Abstract

The factors that control the distribution of diverse endophyte communities across plant hosts and environmental gradients remain poorly understood. This is especially true for endophyte communities inhabiting inner tree bark, one of the least studied components of the plant microbiome. Our study tests the hypothesis that bark of different tree species serves as a habitat filter structuring endophyte communities, as well as the alternative hypothesis, that bark acts as a passive reservoir that collects a diverse assemblage of fungal spores. We develop means of extracting high quality DNA from surface sterilized tree bark to compile the first culture-independent study of inner bark fungal communities. We sampled a total of 120 trees, spanning five dominant overstory tree species across multiple sites in a mixed temperate hardwood forest. We find that each of the five-tree species consistently harbors unique assemblages of inner bark fungi and that congeneric host trees harbor more similar fungal communities than do more distantly related tree species. Physico-chemical components of tree bark (pH, phenolic content) appear to structure components of these fungal communities. Inner bark fungal communities were highly diverse (mean of 105-180 taxonomic units per tree), and are dominated by putative endophytic Ascomycete taxa. Together, we compile strong support for our hypothesis that tree bark serves as an environmental filter structuring inner bark fungal communities. The role of these ubiquitous and plant specific inner bark endophytic communities remains uncertain, but they may play a role in plant defense similar to other endophytic communities.
SEASONAL DYNAMICS OF MYCOBIOMES ASSOCIATED WITH THE GRASS *PANICUM VIRGATUM* GROWING UNDER CONSERVATION AGRICULTURE CONDITIONS

**MON 47**

Anna Kazarina$^{1,2}$, Keerthi Mandyam$^2$, Ari Jumpponen$^1$, Girish Panicker$^{2,3}$

$^1$Kansas State University, Manhattan, USA. $^2$Alcorn State University, Lorman, USA. $^3$The Center for Conservation Research, Lorman, USA

**Abstract**

Plants are not considered a single organisms, but holobionts comprised of the plant host and its associated fungal and bacterial microbiomes that critically affect the health and biomass yield of the plant. However, only limited information exists on the seasonal microbial dynamics of the microbiomes of the perennial grasses in restoration agriculture systems. *Panicum virgatum* – also known as switchgrass – is a perennial native North American C4 grass that plays an important role in conservation ecology and biofuel production. We studied switchgrass cultivated under principles of conservation agriculture at the Center for Conservation Research, Alcorn State University in Lorman, Mississippi. Our primary goals were to understand the seasonal dynamics of the switchgrass root mycobiome as well as the effects of four switchgrass varieties and two planting densities on the mycobiome composition. We sampled soil and roots six times during the growing season in 2018 from the first leaf emergence in early spring to pre-frost in the fall. We extracted total DNA and PCR-amplified the taxon informative Internal Transcribed Spacer barcode to dissect mycobiome composition. Sequencing of the barcode region will permit testing for differences between soil and root mycobiomes throughout the season as well as testing whether or not the planting densities or switchgrass varieties select for distinct mycobiomes. Presented data will provide a snapshot of the microbiome-informed selection of the optimal varieties or planting densities in the context of conservation agriculture.
Profiling Fungal Communities using Oxford’s MinION™ Nanopore Sequencer: A Mock Community Approach

MON 48

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University of Washington, Seattle, USA

Abstract

The ability of Next Generation Sequencers to multiplex environmental samples has advanced the understanding of microbial ecology. Yet, short sequence reads remain a limitation, which Third Generation Sequencers, such as Oxford’s MinION™ nanopore sequencer, offer the capability to solve. The MinION™ can produce longer rRNA amplicon reads from multiplexed libraries, but the higher error rates remain a concern regarding quality and accuracy of sequence output. To assess the MinION™’s capability in profiling fungal communities, four libraries were multiplexed and sequenced. Three were mock libraries that contained varying ratios of 16 taxa belonging to Basidiomycota, Ascomycota, and Mucoromycotina. The fourth library was a mix of the 16 mock taxa and fungal DNA extracted from root-tips. The data was processed through a pipeline selected for efficient analysis of MinION™ output. When taxa were mixed at equal ratios, the MinION™ returned all 16 mock community members. When a taxon was represented at a lower ratio, it was not recovered or decreased substantially in relative abundance. It also profiled the fungal root-tip community, while recovering 14 mock members. Bias was observed among relative abundances, but consistency among taxa mixed at equal ratios remained high. Although the MinION™ has higher error rates, highly accurate consensus sequences (≥97%) can be derived from the longer amplicon reads. This experiment resolved all mock members, inferred community patterns, and identified fungi from a root-tip community, demonstrating that the MinION™ provides a practical alternative for determining fungal community diversity.
Endophyte communities in leaves of tropical angiosperms: the relative importance of foliar defenses, forest characteristics, host relationships, and climate

MON 49

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Abstract

Endophytic fungi that live within healthy leaves protect plants against pathogens and alter leaf water relations. They are transferred horizontally as airborne spores and hyphae, forming communities thought to be structured by factors such as host traits, biogeography, and environmental factors. We examined the relative importance of constitutive chemical and physical defenses of leaves, forest characteristics, host relationships, and climate on endophyte community structure along an elevational gradient in the neotropics. We collected fresh leaves from 120 individual plants across six sites in western Panama, including lowland, pre-montane, and montane tropical forests along a rainfall and seasonality gradient from the Pacific Ocean to the Caribbean Sea. Together these plants represented 48 families and 79 species of angiosperms. We quantified chemical defenses (tannins, phenolics, flavonoids) and physical defense (leaf mass per area) for each leaf and measured endophyte community structure by sequencing the fungal ITS1 region via Illumina MiSeq. Chemical defenses were negatively associated with endophyte richness, but climate and forest characteristics were more informative than chemical defenses alone. Variation in endophyte community structure was not explained robustly by host family or leaf defenses per se; instead, climate and forest characteristics had more explanatory power. We found a positive correlation between species richness and the proportion of locally unique endophytes in each site, suggesting that local-scale processes are important in defining endophyte communities. Together these results inform the factors that shape endophyte communities at leaf-to-landscape scales, providing a basis for testing new hypotheses regarding the evolutionary processes underlying their community assembly.
Soil depth, land use legacy, and historical precipitation regime hierarchically structure fungal communities

MON 50

Paige Hansen¹, Terry Loecke¹, Charles Rice², Benjamin Sikes¹

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Abstract

Much of fungal ecological research has focused on how environmental factors at varying spatial scales structure fungal communities. For instance, sites that vary in historical precipitation regime, land use legacy, and soil depth all harbor significantly different fungal communities. Less clear is the relative importance of these components, and how they interact to structure communities at the landscape scale. We took advantage of the steep rainfall gradient (510-1010 mm precipitation annually) and variety of land use histories across Kansas to investigate how historical precipitation regime, land use, and soil depth hierarchically structure fungal communities. Using a nested experimental design, we sampled soils at five depths in an agricultural field, a post-agricultural prairie restoration, and a native prairie at each of three sites located across the precipitation gradient. We then used amplicon sequencing to characterize fungal communities and nested PERMANOVAs to determine which environmental factors most strongly affect communities. Overall, soil depth explained the most variation in fungal communities (30.9%). Land use explained an additional 24.9%, and differences in annual precipitation explained another 17.0%. These results support previous research indicating that soil depth, land use legacy, and historical precipitation regime are critical to community composition. They also demonstrate that differences in communities are hierarchically structured: first by depth, then land use, and lastly by precipitation regime. Ultimately, these results give insight into what environmental components are relatively the strongest predictors of fungal community composition, and provide a clearer picture of how these factors structure fungal communities at the landscape scale.
New fossil evidence of thyriothecial Dothideomycetes from Cretaceous plant cuticles

MON 51

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Abstract

To understand the evolutionary history of a lineage, the oldest available identifiable fossils are needed to calibrate a phylogenetic tree. Rampant convergence in Fungi has made their fossil record difficult to interpret, and as a consequence, ages of splits in the fungal tree of life are difficult to estimate. However, thyriothecia, which are flat spore-producing structures produced mainly by Dothideomycetes (Ascomycota), can be abundant on fossilized leaf cuticles. Thyriothecia evolved independently many times in Dothideomycetes and are well documented in deposits of Eocene age and younger (<45 Ma). To interpret fossils from further back in time, we used a phylogeny comprising 59 extant thyriothecial taxa to find ancestral character state combinations unique to clades. We then searched for thyriothecia on dispersed fossilized plant cuticles from the Early Cretaceous Dutch Gap Canal (dated 125-113 Ma) and sampled fossilized fragments showing signs of fungal colonization. Of fungal reproductive structures on 281 cuticle fragments, we found ~50 thyriothecia that were preserved well enough to be coded for their characters. The fossil diversity we describe includes specimens indicative of the family Aulographaceae and six other morphotypes with character states and combinations never seen in extant thyriothecia. Most common Cretaceous thyriothecia differ substantially from their extant relatives. We show that it is possible to extend fossil evidence of at least some lineages of Dothideomycetes further back in time by surveying fungi on fossilized plant cuticles and integrating comparative anatomy and phylogeny to guide their interpretation.
Novel endophytic taxa within the Pleosporales and their influence on plant growth

MON 52

Xiomy-Janiria Pinchi-Davila¹, Maria-Jose Romero-Jimenez¹, Ari Jumpponen², Jennifer Rudgers³, John M Dunbar⁴, Cheryl R. Kuske⁴, Andrea Porras-Alfaro¹

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Abstract

Grasses in desert ecosystems experience stressful abiotic conditions including drought and heat and are abundantly colonized by dark septate endophytic fungi. These fungi occur worldwide and include species from multiple orders of the phylum Ascomycota including Pleosporales. Prior work has suggested these endophytes are critical for plant survival and adaptation to drought. We described and characterized a novel group of isolates; further experiments will evaluate their effects on host plants under drought. Fungi were isolated from roots of three native grasses distributed across 18 sites spanning replicated latitudinal gradients in the US. Isolates were characterized using ITS rRNA and LSU rRNA gene sequencing. We compared sequences against the NCBI database and performed phylogenetic analyses using MEGA7. Cultures were also morphologically characterized using different media and growth conditions. Colonies on MEA grew >35 mm diameter in 14 days, presented very diffuse, aerial white mycelium and appeared white, brown, or beige on the underside of the colony. Some colonies on PDA were brown, olivaceous, or beige and stained the media. Isolates had dark septate melanized hyphae when mycelium was older than >14 days. Chlamydospores were found in the mycelium, terminal or intercalary, sometimes solitary; smooth cell wall and oil-droplets characterized the dark hyphae. These novel isolates likely belong to the family Montagnulaceae and are likely closely related to the genera Kalmusia and Didymocrea, representing a candidate new species. However, additional genes will be sequenced to confirm its placement relative to known taxa.
Multigene Characterization of *Darksidea* Isolates and Description of a New Species

**MON 53**

María-José Romero-Jiménez, Ari Jumpponen, Jennifer Rudgers, John M. Dunbar, Cheryl R. Kuske, Andrea Porras-Alfaro

1Western Illinois University, Macomb, USA. 2Kansas State University, Manhattan, USA. 3University of New Mexico, Albuquerque, USA. 4Los Alamos National Laboratory, Los Alamos, USA

**Abstract**

Dark septate fungi in the genus *Darksidea* have a broad distribution across the south-central United States and have been isolated from multiple species of grasses as root-colonizing fungi. However, phylogenetic characterization and ecological roles of species within the genus remain yet to be determined. The objective of this research was to characterize a culture collection of *Darksidea* isolates using a multi-gene phylogeny. Roots of six grass species were sampled across the US. Seventy-seven *Darksidea* isolates were recovered from grass roots and were clustered into eight taxonomic operational units (OTU) based on a 97% similarity of the ITS region. Actin (ACT), β-tubulin (BTUB), calmodulin (CAL) and transcription elongation factor (TEF) genes were PCR-amplified and sequenced to characterize phylogenetic relationships among the *Darksidea* OTUs. Morphology of representative isolates of each OTU was described and recorded using different media (MEA, PDA, SNA, MMR, DG18, WA, CDA, Soil agar, Leonian agar, Emerson agar). Most of the *Darksidea* isolates were recovered from blue grama (*Bouteloua gracilis*), black grama (*B. eriopoda*), or buffalo grass (*B. dactyloides*) from Texas or New Mexico. Six clades were identified; five of them were closely related to *Darksidea* isolated from grasses in Hungary or in the southwestern USA, whereas one represents a candidate new species. *Darksidea* isolates produced a variety of pigments, metabolites, and microscopic structures including chlamydospores, conidia and hyphal coils. *Darksidea* is broadly distributed in arid plants and in the northern hemisphere, indicating potential roles for promoting plant growth in arid environments.
Canker, decay, and entomopathogenic fungi associated with emerald ash borer galleries.

**MON 54**

Benjamin Held, Sofia Simeto, Nick Rajtar, Alissa Cotton, David Showalter, Kathryn Bushley, Robert Blanchette

University of Minnesota, St. Paul, USA

**Abstract**

The emerald ash borer (EAB) is an exotic forest pest that continues to kill millions of ash in the United States and Canada, costing billions of dollars. The beetle was first detected in Minnesota in 2009 and is spreading across the state. The larval stage of EAB creates wounds on trees as they feed on the inner bark causing disruption of water and sap flow, resulting in tree death. The fungal community associated with EAB larval galleries is poorly understood and the role they play in tree death is not known. This study describes fungi isolated from EAB larval galleries sampled throughout the main geographic areas of MN where ash are affected by EAB. Cultures were identified by extracting genomic DNA and sequencing the ITS region of rDNA. Results from 1130 isolates reveal a diverse group of canker, decay, stain, and entomopathogenic fungi. The most common canker associated genera were *Valsa*, followed by *Phaeoacremonium*, *Paraconiothyrium*, *Nectria*, *Diplodia*, *Botryosphaeria*, and *Nothophoma*. Investigations are underway to determine the role of these fungi in contributing to ash mortality in EAB attacked trees. Pioneer colonizing wood decay fungi are also present including species of *Irpex*, *Peniophora*, *Phlebia*, and *Ganoderma*. These fungi have serious implications to urban trees with the potential to cause rapid wood decay that poses hazardous situations. *Purpureocillium* was the most commonly isolated entomopathogen. Others included *Beauveria*, *Clonostachys*, *Akanthomyces*, *Cordyceps*, *Paecilomyces*, and *Pochonia* species. Further studies will explore their potential use as a biocontrol for EAB.
A twenty-year morphological and molecular study of macrofungi in the Driftless area of southwestern Wisconsin, USA.

MON 55

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Abstract

Southwestern Wisconsin comprises the majority of the Driftless area, a geographic region unaffected by Pleistocene glacial drifts that ended some 10,000 years ago. Centered on the Mississippi River, this region’s forests, prairies, wetlands and grasslands support a diverse array of organisms. Over the past twenty years, surveys of macrofungi have been conducted in three older growth forests; these surveys have obtained approximately 1200 species, including some species with disjunct geographical distributions. Despite the high numbers of fungi documented, the proximity of the study sites, and similar dominant tree species between two of the sites, only a 25% species overlap between all three sites was observed. Preliminary DNA sequence data suggest that, because of its isolation, the Driftless area may be home to Appalachian relict species (e.g. Boletus frostii and Ciboria americana) and cryptic species. We are currently using dual-tagged Illumina sequencing in an attempt to economically obtain DNA barcode sequences for nearly 1200 samples; these data will contribute to a better understanding of the geographic distribution and evolutionary history of Driftless area macrofungi. The large scope of this study in terms of survey duration and number of samples offers the opportunity to assess patterns of rarity and endemism of fungi in this region, as well as potential changes in species diversity or composition over time.
2019 Continental MycoBlitz – A New Model for Biodiversity Surveys

MON 56

Stephen Russell, M. Catherine Aime
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Abstract

The North American Mycoflora Project (www.mycoflora.org) is a collaboration between professional mycologists, citizen scientists, online data repositories, and herbaria to document the biodiversity of macrofungi across North America. The cornerstone of this initiative is the documentation, vouchering, and DNA sequencing of macrofungal collections. In order to foster broad citizen science participation in the project, a week-long, continental-scale online foray is being conducted from August 12-19, 2019, with a focus on collecting specimens from under-represented regions and taxonomic groups. As an outcome of this effort, it is expected that over 500 participants across the U.S. will contribute over 20,000 new observational reports to iNaturalist. More importantly, over 2,500 specimens of macrofungi will be vouchered in herbaria; the majority of these specimens will be sequenced utilizing the fungal DNA barcode (nrITS). Proof-of-concept for online forays was conducted at the state-wide level across Indiana in 2017 and 2018, resulting in over 60 participants collecting 1,000+ vouchered specimens that are connected to DNA sequences in public repositories. In this presentation we will discuss the goals and proposed methods for the 2019 Continental MycoBlitz, including considerations for selecting specimens, training regimes for participants, and ways to meaningfully engage citizen populations in fungal biodiversity surveys.
Isolation of Airborne Haloalkane-Degrading Fungi from Puerto Rico

MON 57

Yaisha Vega, Stephanie Nieves-Hernández, Janmary Colón-Alicea, José R. Pérez-Jiménez
Universidad Ana G. Méndez, Recinto de Gurabo, Gurabo, Puerto Rico

Abstract

Halides (haloalkanes) are persistent organic pollutants in water, sediments and soil. Chlorinated and brominated halides are colorless, flammable and toxic liquid compounds. They are commonly found in pesticides, herbicides and industrial solvents. Exposure to these toxic compounds pollutants is probable. Therefore, biodegradation must be considered, because it is more viable and economical way to transforming them into less harmful or non-hazardous compounds. Recently, an aerobic degradation pathway of bromoalkane was described for the yeast Yarrowia lipolytica 3589. Until now, this only yeast reported that can degrade it. Our objective is isolate putative fungi capable of degrading chloro- and bromobutane. 1-bromobutane and 1-chlorobutane were added independently to mineral media as the only carbon source on agar plates. These plates were randomly exposed to air from different places in Puerto Rico and incubated at room temperature. After ten days, small fungal colonies were observed for three sites in the mineral media amended with 1-chlorobutane (~5%). The microscopic examination revealed isolates that presented fine mycelia septa and conidiophore arrangements resembling different strains of Penicillium and Aspergillus. Also, a yeast was found. The characterization is in progress to demonstrate chemical transformations and sequence. Neotropical ecosystems have provided fungi with diverse capabilities that can be useful in the remediation of contaminated sites and preserving public health. As a future objective is intended to propose strategies for the decontamination of this haloalkanes.
Metabolomic analysis reveals new secondary metabolites produced during interactions between strains of *Cryphonectria parasitica*, the American Chestnut Tree Blight.

**MON 58**

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¹Carleton University, Ottawa, Canada. ²Agriculture and Agrifood Canada, Ottawa, Canada

**Abstract**

During the normal course of growth by filamentous fungi, hyphal cell fusion or ‘anastomosis’ between genetically distinct conspecifics can occur. However, a form of programmed cell death called ‘vegetative incompatibility’ (VI) will rapidly follow fusion in interacting hyphae if the two strains are incompatible due to differences at specific vic loci. VI is poorly understood at the cellular level, despite having severely limited the success of viral biocontrols to slow the growth of *Cryphonectria parasitica*, which is estimated to have destroyed over 4 billion mature american chestnut trees over the last century. This study follows a transcriptome analysis of VI in *C. parasitica*, in which several upregulated genes were associated with the production and regulation of secondary metabolites, some with sequence similarity to toxin synthesis genes in other fungi. Using liquid chromatography coupled to high-resolution mass spectrometry, we detected statistically significant shifts in secondary metabolite production during VI interactions, measured over an eight-day time course after co-inoculation of incompatible strains. Following purification and NMR structure elucidation, new molecules related to the known natural product “calbistrin” were elucidated and linked to one of the upregulated biosynthetic gene clusters. This molecule is similar in structure to lovastatin and is currently being evaluated for associated biological activity. Additional metabolomics signals significant to VI match known compounds from fungi and will be discussed. These findings suggest a complex response to VI involving both membrane-associated and secreted molecules, and furthers our understanding of how genetic individuality in *C. parasitica* is maintained.
Unraveling brown rot decay mechanisms to enable the use of a reactive oxygen species (ROS) mechanism

MON 59

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Abstract

Brown-rot fungi are pervasive wood decomposers. Unlike white-rot fungi that use oxidoreductases to degrade lignin extensively to access cellulose, brown rot fungi circumvent the lignin barrier by modifying and cleaving lignocellulose. These modifications have been associated with the production of reactive oxygen species (ROS) via a Fenton reaction mechanism. To generate ROS, two conditions need to be met. First, the concentration of $\text{H}_2\text{O}_2$ and $\text{Fe}^{2+}$ has to be regulated precisely in the extracellular environment. Secondly, the fungus should limit the production of antioxidant compounds that could quench any radicals generated in the first place. To evaluate the potential for an oxidative environment, we analyzed the concentration and ratio of $\text{H}_2\text{O}_2$ and $\text{Fe}^{2+}$ along wood decay using a wafer culture system with Postia placenta. We found that ROS production is only favored at early stages of decay, while inhibited at late stages. This result is the combination of favorable $\text{H}_2\text{O}_2$:Fe$^{2+}$ ratios and the confinement of antioxidant activity only to advanced decay stages. Finally, we identified 3 enzyme groups ($\alpha$-L-arabinofuranosidases, $\alpha$-D-galactosidases, and pectinases) that were expressed early during wood decay in P. placenta, and that showed tolerance to an in-vitro generated oxidative environment. These results were striking, considering the lack of tolerance evidenced in enzyme extracts obtained from Trametes versicolor and Trichoderma reesei, a white-rot and soft-rot, respectively. This behavior might indicate that P. placenta not only is tightly controlling the oxidative potential of its surroundings, but also protecting side-chain hemicellulases expressed during early wood decay.
The Potential Role of Atoxigenic A. flavus Extrolites in Biocontrol Efficacy

MON 60

Geromy Moore, Matthew Lebar, Carol Carter-Wientjes

USDA-ARS-SRRC, New Orleans, USA

Abstract

A preferred pre-harvest strategy to prevent aflatoxin contamination of important susceptible crops involves field application of naturally-occurring non-aflatoxigenic strains of A. flavus. Potential mechanisms by which A. flavus biocontrol strains have been suggested to mitigate aflatoxin contamination include competitive displacement, nutrient sequestration, and thigmoregulation (i.e. touch inhibition). What has yet to be investigated is the potential role of secreted metabolites (extrolites) that could turn off aflatoxin production. We sought to identify putative compounds secreted by an atoxigenic A. flavus strain, and test their ability to reduce growth and/or mycotoxin production for three toxigenic strains (A. flavus L-strain, A. flavus S-strain and A. parasiticus) sampled from the same geographic location. Our study involved several types of solid and liquid medium experiments, for which each medium had been first exposed to several days of growth by the atoxigenic strain prior to re-inoculation with each of the toxigenic strains. Although fungal growth was not always reduced, our findings indicate that the atoxigenic strain secretes at least one extrolite onto/into its substrate that results in a reduction of aflatoxin and cyclopiazonic acid concentrations. This is because no physical contact was permitted between the strains (i.e., no thigmoregulation), and because regular supplementation with fresh liquid medium negated the potential for nutrient sequestration. Through the identification of inhibitory extrolites it may be possible to screen candidate biocontrol strains for enhanced production of these compounds. Furthermore, isolation of these extrolites may also lead to a supplemental post-harvest treatment strategy to maintain inhibition of aflatoxin contamination.
Remediation of metals by Mn-oxidizing fungi in Soudan Iron Mine

MON 61

Tingying Xu$^{1,2}$, Cara Santellli$^{1,2}$

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Abstract

Manganese (Mn) oxides are ubiquitous minerals that commonly control the uptake and release of metals and nutrients. In nature, the oxidation of Mn(II)aq to form the sparingly soluble, nanocrystalline Mn(III/IV) oxides is largely driven by microbial activities. These biogenic minerals are highly reactive and can act as natural sponges to adsorb many metals from the water. For bioremediation, fungal Mn oxides are of particular interest because diverse Mn-oxidizing fungi can thrive in harsh environments and are prevalent in many metal-polluted sites. The Soudan Underground Mine, a former iron ore mine in northern Minnesota, emits wastewater containing high concentration of heavy metals and salts. Nickel (Ni) and cobalt (Co) are the major concerns in the wastewater and are actively being treated at great expense to the mine and State of Minnesota as it has been designated a state park. Thus, a cost-effective bioremediation strategy is valuable, but this requires the understanding of the interactions among metals, fungi, and Mn oxides. We have isolated three fungi (phylogenetic analysis is currently ongoing) from the mine wastewater, all of which are capable of oxidizing Mn(II) to form Mn(III/IV) oxides. We are conducting a series of experiments with fungal cultures grown under high salt conditions with various amount of Mn/Ni/Co. Elemental and spectroscopic analysis will be combined to determine the metal removal mechanisms. Results from this study will directly inform the development of a fungal bioreactor for removing these metal contaminants from high salt wastewaters.
Antioxidant and Antibacterial Activity of High Molecular Weight Polysaccharides and Low molecular Weight Compound Extracted from *Trametes polyzona* (Pers.) Justo Collected from the Wild in Nigeria

**Abstract**

*Trametes polyzona* is a white rot fungus with potentials medically and biotechnologically. The antioxidant and antibacterial activities of high molecular weight polysaccharide extract and low molecular weight subfraction extracted from secondary metabolites produced by the white rot fungus *Trametes polyzona* was investigated. The current study demonstrates that the low molecular weight subfraction exhibited stronger antioxidant and antibacterial activity than the high molecular weight polysaccharide. The low molecular weight subfraction had a combination of low molecular weight polysaccharides and polyphenols. The half maximal inhibitory concentration of DPPH radicals varied from 4.63mg/ml to 19.15mg/ml with the high molecular weight polysaccharide subfraction from *T. polyzona*. The low molecular weight fraction showed higher free radical (1, 1-diphenyl-2-picrylhydrazyl) scavenging activity with EC50 varying from 2.28mg/ml to 6.75mg/ml. Antibacterial activity of the test extracts was evaluated with different strains of bacteria: three strains of *Escherichia coli*, four strains of *Klebsiella pneumoniae*, two strains of *Staphylococcus aureus* and one each of *Salmonella enterica*, *Listeria monocytogenes*. The minimum inhibitory concentration (MIC) for the low molecular weight sub-fractions viz- *E. coli*, *K. pneumoniae*, *S. aureus*, *L. monocytogenes* were 12.5mg/ml, 30mg/ml, 20µg/ml, 50mg/ml and 10mg/ml respectively. The minimum inhibitory concentration for the high molecular weight polysaccharide extract against *K. pneumoniae* was also 50mg/ml. The high molecular weight polysaccharides and low molecular weight fractions from the tissues of *T. polyzona* have potentials as antioxidants and antimicrobial agents.
Fungal enzyme exo-proteome is an important part of phenotype and an integrated part of speciation

MON 63

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Abstract

Secreted fungal enzymes are instrumental for organismal interaction with environment, substrate and host. Secreted, metabolizing enzymes provide nutrients for the species to grow and propagate. Profiles of secreted enzymes have not been used extensively in mycological studies. Interestingly, exo-metabolites such as mycotoxins have been an integrated part of numerous ecological and taxonomic studies. Recently, profile of secreted enzymes were used as an integrated part of the description of the new species (Aspergillus hancockii) from Australia. The presentation will include a description on how enzyme secretome composition can be described, by focusing on enzyme functions and not just based on assigning enzymes to protein families. To achieve this the CUPP method, providing an automated peptide-based functional annotation of carbohydrate active enzymes are used, providing a short-cut from genome sequence to generating an overview of predicted enzyme functions being encoded for in the genome. Furthermore, a CUPP analysis can be complemented by testing enzyme activity; and combining it with a mass-spectrometry of the culture-broth. The understanding of a species enzyme portfolio can provide basis for unravelling its physiology and ecological role, as it reflects fitness of the species, relevant for both growth and reproduction. The evolutionary pressure on speciation is acting on the aggregated metabolizing enzymes -not on type of protein families the enzymes belong. Furthermore, annotating enzymes to function directly from sequence can contribute to unravel evolutionary/ecological concepts by relating enzyme portfolio to organismal taxonomic position. Such increased understanding of fungal species can be improved by including both exometabolome and exoproteome.
DNA Methylation and Gene Expression During Heterokaryosis in the Mushroom Forming Basidiomycetes

MON 64

Rob Powers, Timothy James
University of Michigan, Ann Arbor, USA

Abstract

DNA methylation of cytosines, a well-known form of ‘epigenetic’ modification, has been shown to be important for development and gene regulation in multicellular eukaryotes. Despite the importance and apparent conservation of DNA methylation across diverse clades of eukaryotes, we still lack a basic understanding of its roles in the mushroom-forming fungi of the Basidiomycetes. Recently, it has been shown that the Basidiomycetes have relatively high levels of DNA methylation, and that this modification of cytosines can be found across long stretches of the chromosome, often stretching across thousands of base-pairs. These clusters of epigenetic DNA modification, termed “methylated cytosine clusters” (“MCCs”) appear to be unique to fungi and present most commonly in the Basidiomycete lineage. However, their role in development and gene regulation remains unknown. Here, using a combinations of whole-genome bisulfite sequencing (“WBGS”) and mRNA-seq, we show that in the mycelia of five taxa of the Agaricomycotina (Coprinopsis cinerea, Heterobasidion irregulare, Wolfiporia cocos, Coprinellus disseminatus and Cyathus stercoreus) patterns of DNA methylation and gene regulation change during heterokaryosis. However, most of these DNA methylation changes occur within MCCs, and the presence of high-levels of methylation is correlated across the MCCs with lower gene expression. The apparent repression of transcription of genes within MCCs suggests that DNA methylation is active in silencing gene expression, and not simply functioning as genome. Lastly, we will discuss the content and function of genes that show this coordination of regulation in mycelia during heterokaryosis.
Brown rot fungi - efficient carbohydrate-converting machinery with targeted arsenals

MON 65

Jiwei Zhang\textsuperscript{1}, Claudia Schmidt-Dannert\textsuperscript{1}, Igor Grigoriev\textsuperscript{2}, David Hibbett\textsuperscript{3}, Young-Mo Kim\textsuperscript{4}, Jonathan Schilling\textsuperscript{1}

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Abstract

Brown rot fungi are efficient carbon source converters in terrestrial system, and their mechanisms for deconstructing lignocellulose offer pathways with industrial relevance. These fungi can be found in multiple \textit{Agaricomycotina} linages, which yet convergently evolved the common ability to selectively metabolize carbohydrates of wood (carbohydrate selective; lignin-rich residues). Comparative genomics have revealed that brown rot fungi lost \textasciitilde{}50-60\% functional CAZY genes that were developed in their white rot relatives (simultaneously decay; lignin-poor residues). This in contrast resulted in an enhanced wood-decomposing capacity in brown rot, indicating an updated system that may have been developed in them. Using newly arisen system biology approaches, we are uncovering the genetic mechanisms that underline this brown rot adaptation. Our functional genomics analyses repeatedly supported a unique brown rot “two-step” mechanism that has been adopted widely by fungi to rewire the genetic elements to selectively extract carbohydrates in a highly efficient way. To more systematically understand brown rot, we recently proposed to study the driving forces of brown rot evolution through functional phylogenomics, as well as to build the regulatory network through system biology approaches. We hope these works can help to reveal the sophisticated brown rot controlling system and provide novel views for developing next generation biofuels and bioproducts.
Genomic signatures of host specificity in Ectomycorrhizal fungi

**MON 66**

Lotus Lofgren\(^1\), Rytas Vilgalys\(^2\), Nhu Nguyen\(^3\), Hui-Ling Liao\(^4\), Karrie Barry\(^5\), Igor Grigoriev\(^5\), Alan Kuo\(^5\), Peter Kennedy\(^1\)

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**Abstract**

Ectomycorrhizal (ECM) fungi range in their patterns of host specificity from widespread generalists to genus specific specialists. One of the best documented examples of high host specificity involves fungi in the genus *Suillus*, which primarily associate with plants in the family Pineaceae (particularly the genera *Pinus*, *Larix* and *Pseudotsuga*). Here, we use a comparative genomics approach to identity and investigate the putative genetic correlates of ECM fungal host specificity. Our study contains two parts including 1) contrasting 20 genome sequenced *Suillus* species with 10 ECM host generalist species and 2) a within-*Suillus* comparison contrasted by host group identity. In addition to a broad comparative assessment of gene content, we targeted four suites of molecules which have been shown to be consistently upregulated during the process of host colonization: G-protein coupled receptors, small secreted proteins, transporters, and various secondary metabolites. Comparative genome analysis revealed significant differences in both gene content and context among *Suillus* fungi, including enrichment over other ECM species in secondary metabolite genes overall, driven primarily by a diversity of terpene synthases, as well as significant enrichment of specific classes of G-protein coupled receptors. Due to recent genome sequencing efforts, *Suillus* is proposed as a model for host specificity research, and these results offer new targets for understanding how host specificity may be regulated at the genome scale.
H2A.Z is a multifunctional histone variant that defines distinct promoter classes in eukaryotes

MON 67

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University of Georgia, Athens, USA

Abstract

The histone variant H2A.Z is core structural component of eukaryotic genomes and is highly conserved across fungi, plants, and animals. In vertebrates, H2A.Z is essential for organismal development, and altered function of this histone variant has been linked to human diseases including cancer. H2A.Z has been implicated in numerous biological functions including DNA repair, chromosome segregation, and transcriptional regulation, yet how H2A.Z carries out different functions in distinct genome contexts is poorly understood in any eukaryote. In the model eukaryote Neurospora crassa, H2A.Z is encoded by a single, nonessential gene, enabling genetic and genomic analyses to investigate context-specific functions of this conserved histone variant. As in higher eukaryotes, N. crassa H2A.Z is required for transcriptional activation or repression of numerous genes. We have found five distinct promoter structures in N. crassa using combinatorial clustering of H3K27ac, H3K36me3, and H2A.Z. We will summarize our findings on the impact of these different structures.
Karyon: A bioinformatic toolkit for the analysis of problematic genome projects

MON 68

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Abstract

Recent developments in sequencing technologies and bioinformatics tools have made genome sequencing and assembly accessible to many groups. However, the process of genome assembly can be challenging due to some intrinsic properties of the genome such as high heterozygosity, or the presence of polyploidiés, aneuploidiés, or heterokaryosis. Due to lack of expertise or appropriate tools, many such cases are likely to go unnoticed, potentially resulting in low quality assemblies being nevertheless deposited in public databases. Here we present Karyon, a python based toolkit that aims to help researchers to understand the overall architecture of a de novo genome assembly. Karyon generates a set of plots that can be used to understand the genomic structure of a problematic organism, which in turn might provide an interesting glimpse into its biology and guide researchers towards the use of more specialized approaches.
An Oral History for Mycology #2

POSTER 85

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Abstract

Thirty-one mycologists were interviewed at IMC 11 in San Juan, Puerto Rico. Seventeen women and 16 men from more than 20 countries discussed experiences from the beginning of their careers to the changes over up to four decade careers. They included a husband and wife with independent careers, four former presidents of IMA, the former editors of four mycological journals, the keynote speaker, authors of 400 papers, students beginning their mycological training, a trio of Latinas who pursue mycology enthusiastically, a mycologist who discovered an entire group of previously unseen fungi, and retired mycologists who just can’t quit. We learned a number of accomplished mycologists were the first in their families to go to university, many mycologists found the field accidently, and refugees from flooding had to leave home to continue research. We were reminded of the long history of mycology in Italy and a more recent legacy in Brazil. A human pathogen widely distributed in the harsh environment of dishwashers was discovered by a mycologist at home recovering from ‘flu, and Denmark has a “mouldy phone” number to consult about household fungi. We learned directly from a Congress organizer how to persist and organize an amazing meeting in less than a year after a disastrous hurricane. Time ran out in San Juan, but fortunately we will continue interviews at the MSA meeting. Please sign up for your interview in Minneapolis! (Supported by the LSU Boyd Professor Research Fund)
Molecular and ultrastructural evidence that a pathogen of an agriculturally important green alga belongs in a new lineage of Chytridiomycota

POSTER A1

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Abstract

The green alga *Haematococcus pluvialis* (Chlorophyta) is grown commercially for human and animal dietary supplementation and enhancing marketability of farm-raised salmon. Chytrid fungi are known pathogens of *Haematococcus* in monoculture, and JEL916 was recently isolated into pure culture from a farm in southwestern United States. This monocentric chytrid fungus initially grows epibiotically on individual host cells, later extending elongated rhizoids to other host cells; these rhizoidal extensions also occur in pure cultures on nutrient agar with no host present. Aside from a thickened initial rhizoidal axis, rhizoids are thin and isodiametric. Zoosporangia can mature within 3 days, producing 1–2 raised, inoperculate papillae; zoospores are spherical in motion and contain 1–3 lipid globules. Resting spores develop associated with host cells in senescent *Haematococcus* cultures but not on nutrient agar. In a phylogenomic analysis of currently available taxa, JEL916 was most closely affiliated with a member of the Lobulomycetales. Compared to lobulomycetalean chytrid fungi, however, zoosporic ultrastructure of JEL916 differs in its possession of (1) a small striated inclusion, (2) a rumposome over a lipid globule, (3) a variation of morphology of the flagellar plug, and (4) an array of microtubules densely populating a site proximal to the kinetosome. We will describe JEL916 as a new lineage within the Chytridiomycota; its importance lies both in increasing the known diversity of the Chytridiomycota and in its ability to disrupt agricultural production of an algal monoculture.
The Collection of Zoosporic Eufungi at the University of Michigan (CZEUM): A new culture collection resource unifying 100 years of research.

POSTER A2

Rabern Simmons, Anne Bonds, Buck Castillo, Timothy James

University of Michigan, Ann Arbor, USA

Abstract

We describe a new culture collection resource focused on supporting research on zoosporic true fungi. This collection was founded by aggregating the two most important existing collections into a single resource. Drs. Peter M. Letcher, Martha J. Powell, and Joyce E. Longcore and their students have devoted a combined 100 years of research efforts into amassing culture collections with a focus on the zoosporic eufungi within the Chytridiomycota and Blastocladiomycota. In 2018, we coordinated the transfer of the JEL culture collection of Dr. Longcore (536 isolates representing 10 of 13 described orders including 13 ex-type cultures) from 4 liquid nitrogen Dewars needing weekly maintenance at the University of Maine, to the automated cryopreservation facility at the University of Michigan Research Museum Center. Of 409 non-Batrachochytrium frozen cultures, we have confirmed viability of 252, the majority of which are not identified by molecular methods. Additionally, we recently added 429 cultures (including 23 ex-type cultures) from the University of Alabama Chytrid Culture Collection (UACCC) to CZEUM, making it the largest aggregation of Chytridiomycota and Blastocladiomycota in the world. We have extracted DNA from 249 JEL cultures and have used a MinION Oxford Nanopore Technologies device and R9.4.1 flow cells to sequence multiplexed rDNA amplifications of a 4–6kb region of the 18S-ITS1-5.8S-ITS2-LSU rDNA operon. Comprehensive metadata of the culture collection can be accessed on the website for the Collection of Zoosporic Eufungi at the University of Michigan (CZEUM), and cultures can be supplied for research for a modest recharge rate.
Leveraging genome-wide SNPs to understand the global emergence of the clonal plant pathogenic fungus *Calonectria pseudonaviculata*

POSTER A3

Nicholas LeBlanc\textsuperscript{1,2}, Catalina Salgado-Salazar\textsuperscript{1,2}, Vanina Castroagudin\textsuperscript{1,2}, Jo Anne Crouch\textsuperscript{1}

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Abstract

The clonal fungus *Calonectria pseudonaviculata* is the primary pathogen responsible for the global emergence of boxwood blight, a disease that threatens the production of ornamental plants and the health of native ecosystems. Commonly used genetic markers like microsatellites do not provide enough resolution to study the demographic history or migration of the fungus. The goal of this work was to overcome this limitation through the identification and analysis of genome-wide single nucleotide polymorphisms (SNPs) in global populations of *C. pseudonaviculata*. Fifty isolates of *C. pseudonaviculata* collected from four continents were sequenced using the Illumina MiSeq platform. Sequence data were aligned to a draft genome assembly and initial SNP calls were made using the Genome Analysis Toolkit. Further filtering of SNPs was performed using R packages and BCFtools. Following filtering, 1343 biallelic SNPs were identified across the 54 Mb genome of *C. pseudonaviculata*. Inference of a phylogenetic tree from these data found multiple well-supported genetic clades were present within this species. The majority of isolates from the United States formed a divergent genetic clade, distinct from European and Asian isolates. Only a few *C. pseudonaviculata* isolates from the west coast of the U.S. showed greater genetic similarity to isolates from Europe than other U.S. isolates. Overall, this work demonstrates the utility of using SNPs to study genetic diversity in clonal fungi and provides a means for future investigations into the historical and contemporary migration of *C. pseudonaviculata*. 
What’s for Lunch? Comparative genomics of the *Rhizopus* and allies to test parasitism from saprotrophic background.

**POSTER A4**

Sawyer Masonjones, Jason Stajich
University of California -Riverside, Riverside, USA

**Abstract**

Rhizopus fungi are ubiquitous, saprotrophic pin molds typically found in soil, decaying vegetable matter and dung. Genome sequencing and phylogenomic efforts as part of the ZyGolife project have improved species level phylogenies within the paraphyletic Rhizopus and Mucor genera. Sporodiniella umbellata and Syzygites megalocarpus are animal and mycoparasitic fungi that are sister to the post harvest rot Rhizopus stolonifer. Comparison of these lineages provides an opportunity to examine how transitions in the substrate or host preference is reflected in genomic changes. We sequenced an isolate of *S. umbellata* was cultured from a orb-weaver spider and a *S. megalocarpus* from a mushroom fruiting body infection. Our analysis found Pfam domain and CAZymes content differences between eight Rhizopus, two related Mucor species, *S. umbellata* and *S. megalocarpus* that could be attributed to differences in species ecology. *S. umbellata* have more copies of p450, LRR8, and HLH domains than *R. stolonifer* and encode fewer CAZymes for Glycohydrolases, Carbohydrate Binding Modules, Glycotransferases, and Carbohydrate Esterases. *S. umbellata* lack any pectinases which *R. stolonifer* uses to cause soft rot of fruits. *S. umbellata* also lack mannanases and encodes only one cellulase domain containing protein. These differences may be indicative of its ecology as an insect or arachnid parasite. Across the clade, relative number of protein domains vary greatly. These include Protein kinase, WD40 and the previously described CotH protein family implicated in host invasion. The diverse collection of undescribed CotH containing orthologs which may provide additional targets for understanding Mucoromyoctina fungi host interactions.
Comparative genomics of the entomopathogenic genus *Beauveria*

**POSTER A5**

David Showalter¹, Kathryn Bushley¹, Stephen Rehner²

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**Abstract**

Fungi in the genus *Beauveria* (Cordycipitaceae: Hypocreales) occur worldwide as insect pathogens, plant endophytes, and/or soil-dwelling saprotrophs. Strains of several species are used as mycoinsecticides for the biological control of arthropod pests. The genomic basis of adaption to diverse plant, insect, and soil environments, including the production of an array of secondary metabolites is poorly understood. Moreover, the basis for the origins and maintenance of such diverse ecological capabilities, despite seemingly infrequent sexual reproduction, is unknown. To investigate the genetic basis for this ecological flexibility, the genomes of 12 *Beauveria* species were sequenced, assembled, and annotated. Each genome contained between 9,600 and 11,000 protein coding genes, including 4,984 single copy orthologs found in every genome. The genus-level pangenome is composed of more than 18,000 protein coding genes, with an average of 600 unique proteins per genome. We describe the distributions of carbohydrate active enzymes, proteases, secreted proteins, secondary metabolite biosynthetic gene clusters, repetitive elements, and lineage specific regions of interest in these genomes. The results provide a foundation from which to explore the genomic basis of their flexible life histories and a novel basis for the selection and improvement of applied strains.
Identification and comparison of gene clusters in a diverse collection of 
*Trichoderma* species

POSTER A6

Kelsey Scott¹, Emile Gluck-Thaler¹, Coralie Farinas¹, Guillermo Valero David¹, Zachary Konkel¹, Priscila Chaverri²,³, Jason Slot¹

¹The Ohio State University, Columbus, USA. ²University of Maryland, College Park, USA. ³Universidad de Costa Rica, San Pedro, Costa Rica

Abstract

*Trichoderma* (Hypocreales) is a widespread and diverse genus inhabiting many different environmental niches and is often found in soil and as plant endophytes. Multiple isolates of *Trichoderma* are commercial biocontrol agents, primarily due to strong mycoparasitic capabilities. Mycoparasitism is associated with increased speciation in *Trichoderma* but the evolutionary mechanisms for this are not known. For example, comparison of *Trichoderma* species that have apparently lost mycoparasitic abilities may therefore provide additional insight to the genetic basis of mycoparasitism. Here we report the genome sequencing and annotation of four *Trichoderma endophyticum* isolates obtained from living sapwood tissue of *Hevea* spp. We describe the re-annotation and comparison of 35 publicly available *Trichoderma* genomes from around the world representing a variety of non-exclusive lifestyles (soil-saprotrophy, mycotrophy, endophytism). Using this diverse *Trichoderma* genome dataset we identified genes and gene clusters associated with alternate *Trichoderma* lifestyles and investigated their origin, evolution, and putative functions. We further predicted genomic changes associated with the presumed loss of mycoparasitism in *T. endophyticum* in culture, as well as gene clusters predicted to degrade host defense compounds. This research enhances our understanding of the basis of endophytism and ecological transitions in the *Trichoderma* genus.
Development of a molecular phylogeny of *Hypomyces* to investigate the specificity of the Lobster Mushroom (*Hypomyces lactifluorum* and *Russula brevipes*)

**POSTER A7**

Elizabeth Feliciano, Timothy James
University of Michigan, Ann Arbor, USA

**Abstract**

There have been thirteen species of *Hypomyces* identified that grow on gilled fungi, while two species of *Hypomyces* are known to parasitize mushrooms in the genus *Russula*, *Hypomyces armeniacus* and *Hypomyces lactifluorum*. Although studies have been done that focused on identifying *Hypomyces* species and their hosts using morphological data, no studies focus on building a comprehensive phylogeny that includes all *Hypomyces* species. In this study, I develop a robust phylogeny of the genus *Hypomyces*, focusing on the Lobster Mushroom to study cryptic species and host specificity. The Lobster Mushroom is believed to be *Russula brevipes* that has been parasitized by *Hypomyces lactifluorum*. When inspecting *H. lactifluorum* specimens located at the University of Michigan’s Herbarium, it was clear that the vast number of hosts had not been identified to species. Moreover, the hosts of *H. lactifluorum* have not been identified using molecular data. There are examples where the host has been identified to a morphologically distinct taxa other than *R. brevipes*. Using principal coordinate analysis, I determined if the *Hypomyces* phylogeny shows evidence of cophylogeny between host and parasite, and whether *Hypomyces lactifluorum* is host specific.
Diversity of downy mildews pathogens on Poaceae

POSTER A8

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Abstract

Downy mildew diseases cause significant losses to cereals and grains in many countries every year and represent a threat to crops in the United States. However, our knowledge of the morphological and genetic diversity of the oomycetes responsible for graminicolous downy mildews is limited, which negatively affects our ability to accurately identify, monitor, and quarantine these pathogens in the event of an outbreak. The U.S. National Fungus Collections contains ~300 specimens of globally collected graminicolous downy mildew specimens dating back 1800s that includes 14 species and at least five type specimens. Our primary goal is to use these specimens in combination with specimens from other herbaria to infer a robust phylogeny using mitochondrial (cox1, cox2, and rsp10) and nuclear loci (ITS and LSU).
Three new species of flag smut of grasses from the United States

POSTER A9

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Abstract

Flag smut diseases are widespread on wild and cultivated grasses throughout the temperate and subtropical regions of the world. The pathogens (Urocystis spp., Urocystidales, Basidiomycota) cause a systemic infection on host plants, forming sori in the vegetative parts, most commonly in leaves, and present as narrow stripes between the leaf veins (Mordue & Walker, 1981). Most are believed to have a narrow host range on wild and cultivated grasses (Savchenko et al. 2017). Savchenko et al. (2017) clarified the taxonomy and phylogeny of flag smut pathogens of triticoid grasses using molecular and morphological analyses.

The goal of the present study is to clarify the taxonomy and phylogeny of the flag smut pathogens on several additional grass hosts by analyzing morphological and molecular data. Specimens of Urocystis on several species of Elymus, Schizachne, Bromus, and Poa collected in the United States were examined and analyzed. The results of Bayesian analysis indicate that at least three undescribed species on Elymus, Poa, and Schizachne can be recognized and supported with morphological and host-specificity data. The new species on Schizachne is a first ever record of smut fungi on hosts from this genus. The new species on Elymus from New Mexico falls outside of the major clade of flag smut pathogens of grasses, representing a previously unknown lineage. Several other host-specific lineages were discovered in the phylogenetic analysis that will require additional sampling and further investigations.
Digital imaging of type specimens of rusts and smuts at the U. S. National Fungus Collections

POSTER A10

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Abstract

The USDA-ARS U. S. National Fungus Collections (BPI) contain approximately one million specimens representing all taxonomic groups with a special focus on phytopathogenic fungi. Of these, approximately 25,000 are listed as type specimens. Although label data in text form for more than 800,000 specimens are available online, the specimens, labels and annotations have not been imaged. Rust and smut fungi are particularly amenable to digital imaging for identification purposes, especially when the host plant is known, due to the obvious nature of their infections and the relatively large, ornamented spores that are produced. In 2017, a project was initiated to identify and more completely document type specimens of rust and smut fungi housed at BPI. Following taxonomic assessment, type specimens were annotated and photographed. Images of specimens, packet contents and label information were photographed with a 35mm digital camera. Micrographs of diseased tissue were captured using a dissecting microscope while spores and other microscopic structures were captured using a compound microscope. Annotations will help researchers find type specimens at BPI and the micrographs can be used to identify pathogenic fungi without the need for additional sampling of original material. To date, 1517 type specimens, representing 704 species, have been identified. We present a summary of progress as well as examples of photo documentation generated in this project.
*Fomitopsis mounceae* and *F. schrenkii*—two new species from North America in the *F. pinicola* complex

**POSTER A11**

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**Abstract**

Two new species are described in the *F. pinicola* species complex in North America; *Fomitopsis mounceae* and *F. schrenkii* (Polyporales, Basidiomycota). Previous molecular phylogenetic analyses identified three well-delimited lineages that represent *F. mounceae* and *F. ochracea* from Canada, Appalachian Mountains, and northern USA and *F. schrenkii* from western and southwestern USA. *Fomitopsis pinicola* sensu stricto is restricted to Eurasia and does not occur in North America. Morphological characteristics of basidiocarps and cultures for *F. mounceae*, *F. schrenkii*, and *F. ochracea* are presented. The three species are readily differentiated by ITS1-5.8S-ITS2 (ITS) sequences, geographic distribution, and basidiospore size. *Polyporus ponderosus* H. Schrenk is an earlier illegitimate synonym of *F. schrenkii*. Both *F. mounceae* and *F. schrenkii* have a heterothallic, multi-allelic incompatibility system.
Detecting polyploidy and its role in diversification across *Hydnum* (Cantharellales)

**POSTER A12**

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**Abstract**

Whole genome duplication and gene-loss events leading to changes in ploidy levels are well-characterized in plants and animals. However, the frequency of ploidy changes and subsequent effects on diversification are poorly understood in mushroom-forming fungi. Previous research on the genus *Hydnum* (Cantharellales) has suggested that some species vary in ploidy level and differ by as much as a four-fold increase in chromosome sets. If so, ploidy level could correlate with changes in morphology observed across the phylogeny of *Hydnum*. Here, we present a framework to estimate ploidy levels in *Hydnum* and discuss hypotheses regarding the effect of polyploidy on morphology and diversification in the genus. To estimate ploidy levels in *Hydnum*, we collected dense basidiospore deposits from a range of species to compare relative gene content using flow cytometry. To study the phylogenetic distribution of ploidy level and other characters, we constructed a three-gene (ITS, *rbp2*, *tef1*) phylogeny from more than 50 samples of *Hydnum*, which provides a robust evolutionary framework for comparative analysis.
A new and unusual species of *Hericium* from the Dja Biosphere Reserve, Cameroon

**POSTER A13**

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**Abstract**

Tropical rain forests are the most species-rich biome on the earth. Studies point to the Russulales as the most abundant group of macrofungi in the tropics, but thus far, no member of the Hericiaceae has been described from Africa to our knowledge. Most known species of *Hericium* are from the Americas, Europe, and Asia. Here, we describe a new species of *Hericium* from the Dja Biosphere Reserve (DBR) in Cameroon. The DBR is a biodiversity hotspot with patches of monodominant ectomycorrhizal tree species (*Gilbertiodendron dewevrei* and *Uapaca* spp) scattered along the river banks. Basidiomata were collected during the April–May early rainy season of 2018. The internal transcribed spacer (ITS) and large subunit rDNA (28S) regions were amplified using the primer combination ITS1F/ITS4B and LROR/LR6 respectively. The ITS and 28S sequences were BLASTn and available sequences of other described *Hericium* spp. were downloaded and analyzed for comparison. *Laxitextum bicolor, Dentipellis fragrans* and *D. leptodon* were used as the outgroup. Morphological examination and phylogenetic analysis support the Cameroonian collection as a new sister species to the *H. coralloides* complex. The new species differs from *H. coralloides* by having smaller spores (2.6–3.0 x 1.7–2.2 µm) and longer basidia (up to 27.0 µm). The Cameroon species possesses pleurocystidia, a feature that hasn’t been reported for other members of this genus. The new species like its temperate relatives, likely causes white rot to Congo Basin hardwoods. There is need to increase fungal sampling efforts of biodiversity hotspots such as the Congo Basin.
Many tropical rhizomorphic species of *Marasmius* are not pan-tropical

POSTER A14

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Abstract

*Marasmius* Fr. (Marasmiaceae) is a highly diverse genus of approximately 600 species, with the greatest proportion of its diversity located in tropical ecosystems. Most *Marasmius* species are saprotrophic, meaning their distributions are rarely constrained by host plant distribution. Consequently, some *Marasmius* species are thought to have pantropical distributions. However, the distribution of many tropical fungal species is poorly understood due to fewer collecting efforts in these regions. To better understand the distribution of *Marasmius* species, we sequenced the recommended fungal barcode (the internal transcribed spacer region of the rDNA repeat, or ITS) from approximately 500 *Marasmius* collections from the Neotropics and the Caribbean collected over a 15 year period, and compared them to more recent collections from tropical Africa and Australia. From these data, we have: 1) expanded the known distributions of some *Marasmius* species, 2) provided a DNA barcode for species where one was not previously available, 3) described species that are new to science and 4) elucidated species complexes in this genus. This study provides further evidence that acquisition of vouchered fungal collections with corresponding DNA barcodes provides an invaluable tool not only for taxonomic studies, but for understanding the scope and distribution of fungal diversity. In particular, we found that many rhizomorph-forming species, thought to have a pantropical distribution, actually represent species complexes. These species, such as *Marasmius crinis-equi* and *M. guyanensis*, are character-poor, so species discrimination has been difficult. Ultimately, examination of molecular data from across the entire range of purported distributions is necessary to undertake revision of species complexes in character-poor groups.
New species of *Entolomataceae* from Cameroon

**POSTER A15**

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**Abstract**

Species of *Entolomataceae* (*Agaricales, Agaricomycetes, Basidiomycota*) are found in most lowland tropical rainforests of the world. For tropical Africa, entolomatoid agarics have been comparatively well-documented from certain regions, such as parts of Ivory Coast, Gabon, Kenya, Tanzania, and Uganda, but are largely missing from mycofloristic studies of other areas, including the Congo Basin. Recent collecting activities in the Dja Biosphere Reserve of Cameroon have revealed a rich macrofungal mycota with numerous undescribed species across many agaric families and genera. Here we report on five new species of *Entolomataceae* and a new distribution record for *E. semilanceatum* (Romagn.) E. Horak, previously known only from the Congo. This work represents the first contemporary taxonomic study of the *Entolomataceae* from Cameroon. Macro- and micromorphological characters, habitat, and DNA sequence data of the new species will be presented.
High diversity of milkcaps (*Russulaceae, Basidiomycota*) associated with *Dicymbe* in tropical forests of Guyana

**POSTER A16**

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**Abstract**

Diversity of ectomycorrhizal (EM) fungi in the Neotropics is still relatively poorly known. Tropical rainforests dominate the region, but EM hosts constitute only a fraction of the tree diversity. However, in Guyana some forests are dominated by EM trees of the leguminous genus *Dicymbe*. Over 20+ years, macrofungal collecting in *Dicymbe* forests has yielded a great number of EM taxa. An important group of EM fungi in the *Dicymbe* system are the milkcap mushrooms of the genera *Lactifluus* and *Lactarius*.

Molecular and morphological study of these milkcaps collections revealed a total of 17 species, of which nine are *Lactifluus* and eight *Lactarius*. The *Lactifluus* species are well distributed infragenerically, occurring in three out of four subgenera, and some exhibit unusual characteristics such as a partial veil or a pleurotoid habit. Only three of these *Lactifluus* species have been described so far. For *Lactarius*, eight species have been found in Guyana, a striking fact given that the main center of diversity for the genus is in Northern temperate regions. Seven of these newly discovered *Lactarius* species form an early diverging clade in *Lactarius* subgenus *Plinthogalus*. While this subgenus is predominantly known from the Northern hemisphere, it also contains early diverging African lineages. The discovery of Neotropical taxa in *Lactarius* subgen. *Plinthogalus*, previously thought to have originated in Africa, changes our ideas about the evolution and biogeography of the subgenus and even *Lactarius* as a whole. In addition, this illustrates the importance of including tropical taxa in the study of fungi.
Ectomycorrhizal fungal hyperdiversity revealed in tropical monodominant forests of Cameroon

POSTER A17

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Abstract

The ectomycorrhizal (EM) mutualism remains poorly characterized in tropical habitats compared to temperate and boreal ecosystems. Tropical EM fungi are notably understudied, particularly in the Guineo-Congolian forests of Central Africa. In this study, we report on an ongoing, intensive long-term sampling of the EM fungal community in a monodominant forest of the EM tree Gilbertiodendron dewevrei (Fabaceae subfam. Detarioideae) in southern Cameroon. Systematic, repeated-visit plot-based sampling for EM fungi was conducted yearly over the course of four years. During a season, in each of three 1-hectare permanent plots, fifty 100 m² subplots were exhaustively sampled over a 6-8 week period. Additional collections were made from outside the plots. To date, over 2000 sporocarp collections have been vouchered and ITS-barcoded. Morphological recognition of morphospecies along with operational taxonomic clustering of ITS sequences has revealed nearly 250 EM fungal species. Species accumulation curves indicate that saturation has not been reached, which is corroborated by the large number of unmatched EM OTUs recovered belowground in a separate study. This study highlights the importance of long-term sampling and vouchering of fresh collections within a given ecosystem to begin capturing the full breadth of macrofungal species within a guild. Therefore, we suggest that repeated sampling over multiple field seasons, in combination with DNA-based barcoding, is necessary in order to draw meaningful conclusions about the fungal diversity within a given ecosystem.
New species and epitypes of *Amanita* from Central Africa

POSTER A18

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Abstract

The diverse, primarily ectomycorrhizal (EM) mushroom genus *Amanita* (*Amanitaceae, Agaricales, Basidiomycota*) may have over 1000 species worldwide, with ~600 species formally described. Many *Amanita* species have broad distributions in higher latitude forests, while *Amanita* species in the Afrotropics are geographically restricted in lowland rainforests and woodlands dominated by EM trees of *Fabaceae* subfam. *Detarioideae*. Many African *Amanita* species described in the early twentieth century were based on a single type collection made by Mme Goossens-Fontana in Congolian forests of the EM detarioid *Gilbertiodendron dewevrei*. These species have been infrequently documented, if at all, in subsequent decades. Our collecting expeditions over 2014–2018 in Cameroonian *Gilbertiodendron*-dominated rainforests have yielded at least 40 distinct *Amanita* morphospecies. Some of these are new to science and others correspond to poorly-documented species based on the Goossens-Fontana collections. Here we present macro- and micromorphological characters and multi-locus DNA sequence data for two new species and four species to be epitypified.
**The Great White Amanita: Deciphering the Amanita bisporigera Species Complex Through Toxin Profiling and Phylogenetics**

**POSTER A19**

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**Abstract**

Amanita bisporigera is a pure white mushroom species that is deadly poisonous if consumed, hence its common name, the Destroying Angel. This mushroom species is native to North America and is responsible for human and pet fatalities every year. This mushroom contains lethal amounts of amatoxins and phallotoxins, which inhibit protein synthesis. The presence, composition and concentration of toxins varies across specimen. Recent phylogenetic studies indicate that A. bisporigera is a species-complex, likely consisting of multiple cryptic species. This hypothesis may help explain the wide toxin variability that has been found between mushroom specimen. However, this hypothesis has not been tested directly. To address this hypothesis, we are using multigene phylogenetics to resolve species in the Amanita bisporigera species-complex, and liquid chromatography and mass spectroscopy (LCMS) to test for variation in toxin presence and concentration within and between phylogenetic species. Fresh collections of white Amanita were collected in Michigan during the Fall of 2018 and the Summer of 2019. Each mushroom was flash-frozen and phenotyped for amatoxin and phallotoxin analysis with (LCMS). A multigene phylogeny was build with sequences of Internal Transcribed Spacer (ITS) rDNA, large subunit (LSU) rDNA, ß-tubulin, and RNA polymerase II (RPB2). Toxin profiles will be mapped onto the resulting phylogenetic tree. Our preliminary analysis have identified at least one novel toxic species in this complex, which will be formally described.
Richer than Gold: the fungal biodiversity of a threatened Andean cloud forest reserve.

POSTER A20

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Abstract

Globally, many undescribed fungal taxa reside in the hyperdiverse, yet undersampled, tropics. These species are under increasing threat from habitat destruction by expanding extractive industry, in addition to climate change and other threats. Reserva Los Cedros is a primary cloud forest reserve of ~17,000 acres, and is among the last unlogged watersheds on the western slope of the Ecuadorian Andes. No fungal survey has been done there, presenting a rare opportunity to document fungi in an relatively undisturbed ecosystem in an underrepresented habitat and location. Six above-ground surveys from 2008–2019 resulted in ~1700 vouched collections, mostly Agaricales sensu lato and Xylariales. We document diversity using a combination of ITS barcode sequencing, digital photography, and participation in online citizen science platforms, such as Mushroom Observer. Preliminary identifications indicate the presence of at least 5 phyla, 17 classes, 30 orders, 81 families, and 190 genera within the reserve. Two taxa at Los Cedros have recently been recommended to the IUCN Fungal Red List Initiative (Thamnomyces chocóensis and Callistodermatium aurantium), and we add occurrence data for two others already under consideration (Hygrocybe aphylla and Lamelloporus americanus). Plants and animals are known to exhibit exceptionally high rates of endemism in the Chocó bioregion, but endemism in fungi is poorly understood. Our collections contribute to understanding this important driver of biodiversity in the Neotropics. Mining expansion into protected forests, including Los Cedros, poses an existential threat to the fungi we have observed, and those that have escaped collection.
The *Laetiporus* genus in Brazil

**POSTER A21**

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**Abstract**

Traditionally, Laetiporus genus was comprised of only two species: *Laetiporus sulphureus* (Bull.) Murrill and *Laetiporus persicinus* (Berk. & M.A. Curtis) Gilb. Those two were characterized as brown rot wood decomposers, producing large and soft basidiomata, dimitic hyphal system and white spore print. Both were easy to identify macroscopically with this delimitation. But recently, using molecular tools to test evolutionary trends within the genus, researchers found that *L. sulphureus* was a taxonomic complex hiding tens of species around the world regard their tree host and geographical location and some species that were synonymized to *L. persicinus* could be another genus until undescribed. We reviewed *Laetiporus* specimens in herbaria collections from Brazil and made new ones totalizing 52 basidiomata looking at macroscopic, microscopic and molecular level. All specimens that were in herbaria had the names *L. sulphureus* and *L. persicinus*. We found that those collection identified as *L. persicinus* were wrong interpreted and are from *Polyporus talpae* Cooke, that nowadays is considered a synonym of *L. persicinus* but it is more related to a genus described from Africa, *Kusaghiporia usambarensis* J. Hussein, S. Tibell & Tibuhwa, and need a new taxonomic combination. We found that those identified as *L. sulphureus* are *Laetiporus gilbertsonii* Burds. and that those could be jumping host to Melastomataceae tree, a host that was never described for *Laetiporus* species. Least, we found what seems to be a new species for science growing on *Schinus* sp. tree that’s been described.
Breaking ties to ectomycorrhizal fungi at the arctic treeline: using stable isotope fingerprinting to infer mycorrhizal dependence

POSTER A22

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Abstract

White spruce growth at an arctic treeline may be limited by nutrient availability in cold soils. Ectomycorrhizal (ECM) fungi aid these trees in nutrient acquisition at a potentially high carbon cost. This study aims to examine changes in mycorrhizal dependence with elevation and to test the strength of the tree-fungal association in the face of experimental changes in soil nutrient availability. If fertilization diminishes spruce dependence on ECM fungi, will control trees display amino acid δ¹³C values, or isotopic fingerprinting, intermediate to a fungal fingerprint and the fertilized trees? Secondly, which taxon remain despite fertilization and is mantle development impaired? Roots and needles were collected from fertilized and control trees (n = 60) at three sites along an elevation gradient in northwestern Alaska. Root tips will be assessed for percentage of ECM fungal colonization and root tip architecture to determine mycorrhizal dependence. The 18S rRNA genes of pooled root tips from each tree will be sequenced with an Illumina platform. Needles will be analyzed for nitrogen and phosphorous concentrations to determine nutrient acquisition. Needles will also be analyzed for amino acid δ¹³C values to examine the viability of applying isotopic fingerprinting to mycorrhizal interactions.
How specific is ectomycorrhizal host specificity?

POSTER A23

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Abstract

Fungi in the ectomycorrhizal genus Suillus are widely recognized for their high specificity with tree hosts in the family Pinaceae, which consists of two clades: Pinoid and Abietoid. Although Suillus has only been documented to associate with the former clade, Suillus sporocarps have been found in Pinaceae forests in which no known Pinoid hosts (Pinus, Pseudotsuga, and Larix) are present. To investigate possible alternative host associations, we conducted a growth chamber bioassay using Suillus glandulosus, a species which commonly fruits in both Picea (Pinoid clade) and Abies (Abietoid clade) dominated Canadian forests. Seedlings of Larix laricina, Picea mariana, and Abies balsamea were grown in single- or two-host species pairings and inoculated with high densities of S. glandulosus spores to determine both host association and mechanism of colonization. We found that only L. laricina was colonized after 3 months, while both P. mariana and A. balsamea seedlings were lowly colonized in the two-host treatments with L. laricina after 6 months. These results suggest that while Larix is needed to trigger Suillus spore germination, both Picea and Abies can be colonized by mycelial extension. Results from the final part of the bioassay will also be presented in which colonized Picea and Abies seedlings have been isolated from co-planted Larix seedlings, to determine if alternative hosts can independently support the growth of Suillus. Collectively, these results indicate that Suillus fungi may be able to associate with Abietoid hosts in natural settings and that the classical conceptualization of Suillus host specificity may require revision.
The role of competition in ectomycorrhizal fungi gene expression and host phenotype

POSTER A24

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Abstract

The mutualism between temperate trees and ectomycorrhizal fungi (ECM) dominates much of the northern hemisphere. This association provides numerous benefits for the tree host such as nitrogen acquisition, drought tolerance, and defense. Recent manipulative research has only studied simplified systems with one ECM associate per host, however, ECM soil communities are highly diverse, and hundreds of species may colonize a single tree. Moreover, interspecific competition has been hypothesized to maintain this high alpha-diversity and may significantly alter ECM gene expression. To test these hypotheses we are conducting a novel metatranscriptomic assay that seeks to elucidate the role of belowground competition and phylogenetic relatedness in gene expression of ECM fungi. *Populus tremuloides* seedlings will be grown in the presence of one to several ECM species (1-8) covering a vast array of phylogenetic diversity and ecological habits. mRNA of each ECM will be extracted from ground whole root systems. We will compare the transcriptomes of each ECM species in and out of competitive environments to interspecific competition in ECM. In addition, we are conducting a broad metabolomics survey using UPLC of the host leaves to identify changes in metabolite production due to belowground competition. We hypothesize that competition will have an additive effect on gene expression, where distantly related ECM up-regulate genes associated with nutrient acquisition and transport to become better mutualists, while closely related ECM shift expression to avoid niche competition. This study may lead to insights on the role of competition in ECM niche portioning and host phenotype.
Will the high elevation distribution limits of ectomycorrhizal fungi shift in response to climate change?

POSTER A25

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Abstract

Species distributions are expected to shift to higher elevations and latitudes in response to contemporary climate warming. However, because species appear to be shifting their distributions at different rates, some may reach environments that lack the species with which they usually interact. This may be a significant barrier to distribution shifts in species that depend on mutualistic interactions such as ectomycorrhizal fungi (EMF) and their plant hosts. To begin exploring this hypothesis, we describe the species composition of EMF communities of subalpine fir (*Abies lasiocarpa*) at their high elevation distribution limits. At our study site in Mount Rainier National Park (WA, USA), subalpine fir constitutes treeline and grows in small forest patches or as isolated individuals in subalpine meadows. The isolated trees in meadows are considered to represent the early stages of a climate-warming induced distribution shift for subalpine fir. We predicted that the roots of isolated subalpine fir would harbor only a subset of the EMF found in forest patches due to dispersal limitations and unfavorable abiotic conditions in the meadows. We used morphotyping and ITS sequence data to describe EMF communities in these two environments and quantified relevant soil variables (water holding capacity, C:N ratio of organic matter, inorganic P) at all sampling locations. The results of this study should provide insight into the potential distributional shifts of EMF in response to climate change.
Ectomycorrhizal fungal community development on seedlings of a Neotropical monodominant tree

POSTER A26

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Abstract

Ectomycorrhization is important for early survival of seedlings of ectomycorrhizal (EM) tree species. In Guyanese forests dominated by EM canopy tree *Dicymbe corymbosa* (Fabaceae subfam. Detarioideae), conspecific seedlings experience high multi-year survivorship in crowded, often heavily-shaded environments. Ectomycorrhizal fungi may facilitate seedling survival under these challenging growth conditions. Little information exists, however, on the development of EM fungal communities in seedlings of EM tropical monodominant trees. This is especially true regarding how the extent of EM colonization or community assembly of EM fungi may influence early seedling survival. We sampled an even-aged cohort of seedlings of *D. corymbosa* at < 1, 6, and 12 months following a mast seeding event and determined their percent mycorrhization and mycobiont assemblage for each age class. Cross-generational sharing of EM mycobionts was assessed by comparing seedling EM fungal communities to those of nearby adult conspecifics. Percent mycorrhization did not increase over time, but rather was highest at 6 months, with no significant difference in colonization at < 1 and 12 months. However, species turnover in EM fungal communities over time was high, with only 20% overlap in EM fungal species between 6- and 12-month seedlings. *Tomentella* (Thelephorales) species were particularly abundant in each seedling age class and were also the most abundant in adult trees. This study suggests that the qualitative composition of EM fungal mutualists may play a larger role than the extent of mycorrhization in early seedling survival of tropical monodominant trees.
Legacy of *Robinia pseudoacacia* (black locust) invasion and use of ectomycorrhizal fungi to restore *Pinus rigida* (pitch pine) in the Albany Pine Bush Preserve, NY.

**POSTER A27**

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**Abstract**

Invasive plants can leave lasting legacies on ecosystems, including changes to ectomycorrhizal fungi (EMF). Such legacies can make restoration difficult even after invaders have been removed. Previous research has identified suilloid fungi (*Suillus* and *Rhizopogon*) as important in early pine establishment, making them potentially useful in pine restoration. To test the hypothesis that *Robinia pseudoacacia* has a negative impact on resistant propagules of EMF associated with *Pinus rigida* we carried out soil bioassays with soil from sites where *R. pseudoacacia* had invaded but recently been removed and from non-invaded sites. Bioassay seedlings planted in *R. pseudoacacia* invaded soils had three EMF species compared to five species non-invaded sites. One EMF species was present in both. One suilloid species, *Rhizopogon pseudoroseolus*, was found on seedlings in non-invaded soils. To test the hypothesis that suilloid fungi can improve survival and that *R. pseudoacacia* has a legacy effect on *P. rigida* survival, *P. rigida* seedlings were inoculated with live or autoclaved locally collected suilloids spores and planted in a factorial field experiment (inoculation treatment x invasion history). There was no difference in survival of field seedlings between invaded or non-invaded sites after 8 months. However, 72% of seedlings inoculated with live spore inoculum survived, compared to 31% of seedlings inoculated with autoclaved spores (*P* < 0.001). These results suggest the legacy of *R. pseudoacacia* does not limit restoration of *P. rigida* at the Albany Pine Bush Preserve, but that establishment increases when pines are inoculated with locally adapted suilloid fungi.
Foliar Endophytic Fungi Alter Plant Host Chemistry

POSTER A28

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Abstract

Colonization by fungal endophytes have broad benefits for plants, including increased resistance against herbivores and pathogens. Endophytes in culture have been shown to produce secondary metabolites that can suppress herbivore and pathogen damage. It is unknown if these toxins are also synthesized during symbiosis within the host plant, or if endophytes stimulate plant chemical responses, thus affecting plant interactions with their enemies. We tested how endophyte colonization alters the production of defensive compounds in the toxic plant white snakeroot (\textit{Ageratina altissima}), a native Indiana wildflower. We inoculated endophyte-free seedlings with one of three treatments: 1) inoculation by a single, dominant endophyte (\textit{Colletotrichum} sp.), 2) inoculation with rainwater captured underneath wild snakeroot plants as a natural fungal spore source, or 3) application of sterile water as a control. After endophyte communities established in seedlings, we quantified colonization success using a culture-based approach, coupled with Sanger sequencing. Plants inoculated with rain water had the most diverse endophyte communities. To determine if endophyte community composition and diversity affected plant chemistry, we extracted phenolics from leaf tissue and performed liquid chromatography-mass spectrometry. Comparing the phenolic profiles across the three treatments revealed microbial colonizers alter the production of secondary metabolites in plants. Plants treated with \textit{Colletotrichum} sp. and rain water had a significantly larger breadth of chemical compounds in their tissues than uninoculated seedlings. Additionally, abundance of individual phenolic compounds varied between treatments. Future work will examine if these chemicals were produced by endophytes or were produced by plant pathways triggered by fungal colonization.
Drivers of endophyte communities within Pacific Northwest prairies

POSTER A29

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Abstract

Prairies of the Pacific Northwest are highly threatened systems, with only ~2% of historic land area remaining. The combined risk of global climate change and land use change make these systems a high conservation priority. However, little attention has been paid to the microbiota of these systems. Fungal endophytes are ubiquitous in plants and are important in ecosystem functioning and host dynamics. While emphasis has largely been placed on single, economically relevant endophytes, there are often hundreds of species occupying a single leaf. Despite our poor understanding of the functional role each fungal species plays within these complex systems, community composition may give insight into host-endophyte interactions. Using high-throughput illumina sequencing, we investigated the diversity and composition of fungal foliar endophyte communities in two native, cool-season bunchgrasses along a natural latitudinal gradient. We quantified the relative importance of host, host traits, climate, edaphic factors, and spatial distance in microbial community composition.

We found markedly different communities between the southern and central-northern sites, suggesting a potential dispersal limitation in the Klamath Mountains ($F_{1,153} = 5.080, p < 0.001$). We also found that each host species was home to distinct fungal communities ($F_{1,153} = 5.965, p < 0.001$). Host species, spatial distance and climate were the strongest predictors of endophyte community, while host traits (e.g., plant size, reproductive status, density) were less important for community structure.
Bark Beetle Mycobiome: An International Coordination Group Advancing Bark Beetle Symbiosis Research

POSTER A30

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Abstract

Bark beetles have evolved symbioses with fungi and their tree hosts that range from highly specific, to loose associations, to asymmetrical dependence. Besides contributing to the advancement of symbiosis and evolutionary ecology theories, the beetle-fungus relationship has often been hugely destructive, with outbreaks and epidemics reaching record proportions in forests on every continent, costing billions of dollars per year and damaging important ecosystems. The scientific community working towards understanding and mitigating these emerging global threats is facing a critical shortage of expertise, comprehensive and curated public databases, updated research protocols and standards, and well-established knowledge flow systems that connect a global community of forest entomologists and pathologists. These challenges result in the use of incomplete or incorrect information by end-users who make policy decisions concerning international biosecurity, trade, and natural resources protection. This five-year project aims to coordinate research efforts of forest pathologists, entomologists and symbiologists throughout South Africa and the U.S. With over 22 individual researchers representing 17 institutions in five countries, our objective is to critically assess how bark beetles and their fungal associates are studied and interpreted and identify and recommend ways to improve current research approaches.
Links between ash fungal endophytes and emerald ash borer gut communities?

POSTER A31

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Abstract

The emerald ash borer (EAB), a beetle endemic to northeastern Asia, has invaded eastern North America where it is causing a widespread die-off of ash (Fraxinus sp.). Adult beetles lay eggs on the tree bark and, after hatching, larvae feed on phloem tissue, destroying the tree’s ability to conduct water and nutrients. Microbial symbionts of other phytophagous insects have been shown to play important roles in lignocellulose degradation, breakdown of plant chemical defenses, or in nutrition and development of their insect hosts. There is some evidence to suggest an active fungal community within the EAB larval gut, but the taxonomic and functional diversity as well as drivers of community assembly of this gut microbiome are unknown. Larvae within EAB galleries may acquire a portion of their gut microbiome by consumption of fungi living as endophytes within ash phloem. In order to describe the relationships between EAB gut microbial species and ash endophytes, we conducted culture-dependent and independent community profiling of EAB frass and phloem samples. We also aimed to determine whether any of the fungal taxa isolated from ash phloem or EAB frass potentially aid in EAB’s attack via lignocellulose degradation, detoxification of plant defense compounds, or other nutrient provision mechanisms. Preliminary lignocellulose and phenolic degradation assays will provide insight into the potential biochemical mechanisms within this microbial community to better assess the nutritional ecology of EAB.
Fungal endophytes and their role in herbivory deterrence against an invasive scale insect in the Mississippi River Delta

POSTER A32

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Abstract

With recent focus on both organismal and ecosystem microbiome composition, it is quickly becoming apparent that symbiotic fungal endophytes, those that asymptomatically infect plant tissues, are nearly ubiquitous throughout the plant kingdom providing a variety of services to their plant hosts. One such service is protection from herbivory. *Nipponaclerda biwakoensis*, an invasive scale insect recently discovered in high densities in the Mississippi River Delta (MRD), has been correlated with diebacks of a foundational plant species, *Phragmites australis*. This is of great concern because Louisiana’s coastal marshes are in danger of being lost to sea level rise and erosion and *P. australis* plays an integral role in the mitigation of these threats. Previous work has shown that there is considerable variation in scale infestation among *Phragmites* stands; specifically between two dominant *Phragmites* haplotypes, M and M1. In September 2018, I traveled to two sites in the MRD and collected samples of both haplotypes to assess infestation severity and fungal endophyte composition. My preliminary findings show that haplotype M1 is significantly more infested than haplotype M, and there is also substantial variation in infestation within each haplotype. I hypothesize that differences in infestation between and within haplotypes can be attributed to the presence of mutualistic fungal endophytes which directly and indirectly confer resistance to *N. biwakoensis*. Overall, this work is an important first step in identifying key fungal players in plant-herbivore interactions in an important coastal system, which can eventually be leveraged to enhance restoration in the area.
Hybrid assembly of a novel Zombie Ant Fungus (*Ophiocordyceps*) genome and discovery of candidate manipulation genes in the transcriptome.

POSTER A33

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Abstract

*Ophiocordyceps camponoti-floridani*, a species of “Zombie Ant Fungus,” infects and modifies the behavior of carpenter ants to further its own transmission at a lethal cost to the host. Manipulated ants perform a “death grip” biting and clinging behavior to attach themselves to plants. This novel behavior is understood as a fungal manipulation that benefits the parasite’s growth and transmission. Across the manipulative *Ophiocordyceps*, host modification is often observed at stereotypic times of day, on particular substrates, and in specific host species. The underlying mechanisms of how these fungi can dysregulate animal behavior in such a coordinated manner has yet to be described. Analysis of fungal gene activity across the entire transcriptome at the time of manipulation allows detailed investigations into the fundamental mechanisms used by these fungi. These explorations can then lead to functional testing of potentially key gene products and metabolites. Using a combination of Nanopore and Illumina sequencing technologies, we produced a hybrid assembly of the genome of this species. Subsequently, we performed RNAseq to characterize differential fungal gene expression across the course of infection and manipulation. To select a robust set of candidate “manipulation genes,” we will combine these data with a former gene expression study of *O. kimflemingiae* in a comparative transcriptomics analysis. Strong candidates will then be functionally tested for necessity in manipulated phenotypes, using controlled infections of transgenic knockout fungi with loss of function of the gene of interest.
Are *Cordyceps* secondary metabolite gene clusters involved in insect behavior manipulation?

POSTER A34

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Abstract

Arthropods are an important source of nutrition for fungi, providing numerous niches for diversification of entomopathogens. Entomopathogenic fungi sometimes manipulate insect behavior as part of their spore dispersal phenotype, but the molecular and physiological mechanisms of manipulation are not well understood. Through analyses of clustering of related gene functions in multiple newly generated, Nanopore-Illumina genomes of *Cordyceps s.l.* species, we identified a putative neuroactive gene cluster. What we refer to as the GABA cluster is composed of 5 genes, including homologs of glutamate decarboxylase (GDC), Glutamine Phosphoribosylpyrophosphate Amidotransferase (GPA), and a Nitrate transporter (NRT2). The complete gene cluster appears to be ancestral in *Cordyceps s.s.*, and is retained in *Cordyceps militaris* and *Isaria fumosorosea*, but partially lost in *Beauveria bassiana*. Here we present research whose ultimate goal is to characterize the function and evolution of the GABA gene cluster, and to investigate its possible role in behavior manipulation. We heterologously expressed GDC and GPA for use in enzymatic analyses, and monitored the production of GABA *in vitro* and *in vivo* using liquid chromatography-tandem mass spectrometry. This work represents a significant step in the understanding of neuroactive metabolite production by entomopathogenic fungi.
Investigating ecological trade-offs in endophytic insect pathogenic fungi

POSTER A35

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Abstract

Endophytic insect pathogenic fungi are plant mutualists and insect antagonists and can therefore protect their plant hosts from detrimental insect pests. This study examined trade-offs between being a plant mutualist and an insect pathogen fungus. We assessed the endophytic and pathogenic capacities of 8 isolates of Beauveria and Metarhizium (B. pseudobassiana, B. bassiana, M. anisopliae, and M. pemphigi) to determine if single isolates are better at one strategy than the other. We performed two assays in order to test for the presence of trade-offs. In the insect pathogenicity assay, surface-sterilized wheat stem sawfly larvae were exposed to standardized spore solutions from the Beauveria and Metarhizium isolates. Infection and mortality of the larvae was tracked over a 7-day period. In the endophyte assay, wheat plants were cultivated from seed in a greenhouse and exposed to standardized conidial solutions of each fungal isolate and grown for four weeks. For each plant we measured chlorophyll content, height, and number of shoots, leaves, and inflorescence before and after the treatment. Our preliminary results show all isolates have high efficiency establishing as insect pathogens as we observed rapid and high mortality rates within larvae across all isolates. Wheat plants exposed to distinct isolates within the endophyte assay showed differential growth and physiological characteristics that may be due to endophyte establishment, suggesting a potential trade-off in endophytic pathogenic ability for some isolates. Our next steps include sequencing the fungal ITS region from plant tissue to ascertain endophyte presence and determine differential endophyte establishment and mutualistic ability.
From fungus to flower: Pseudoflower formation on *Xyris* associated with a novel *Fusarium* species from Guyana, and its potential dispersal by insects

POSTER A36

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Abstract

Fusarium is a genus associated with several economically important plant diseases and toxicoses. Some phytopathogenic fungi use mimicry to physically resemble plant structures that attract insects. Fieldwork conducted in western Guyana revealed an abundance of fungus-associated pseudoflowers on *Xyris surinamensis* and *X. setigera* (yellow-eyed grasses). An unusual new species of *Fusarium* was associated with these pseudoflowers, being the first report linking a *Fusarium* species to this phenomenon. Our study aims to 1) characterize the disease caused by this *Fusarium* sp., 2) determine the main dispersal mechanism for the fungus, 3) evaluate the role of pseudoflowers on insect attraction, and 4) determine if pseudoflower production is associated with the presence/absence of other microorganisms. Field observations will determine signs and symptoms produced by the disease. Greenhouse experiments will be used to evaluate infection mechanisms, while field samples will be tested for presence of the fungus on healthy plant tissue, seeds, and rhizosphere soil. Insect visitation studies will identify insects that come in contact with flowers and pseudoflowers on *Xyris*. A nested PCR method will be used to detect *Fusarium* DNA on collected insects. Volatile organic compound (VOCs) production will be compared between infected and uninfected plants to determine if fungal infection generates insect-attracting VOCs. The microbial community composition of pseudoflowers and inflorescences will be compared. Other pseudoflower-inducing fungi have been described, yet connections between disease-induced traits, transmission, and vector attraction require further research. Our study helps elucidate these plant-insect-pathogen interactions by providing understanding of their evolutionary ecology and transmission biology.
Why did the mushroom become magic? – Effects of *Psilocybe cubensis* on possibly antagonistic organisms

**POSTER A37**

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**Abstract**

The serotonin-analog, psilocybin, and its chemical relatives, prevalent in *Psilocybe* species, have poorly understood ecological roles, as do fungal secondary compounds generally. Due to serotonin’s importance in animal nervous systems, these serotonergic compounds could have evolved for defensive purposes. This study investigated the defensive potential of *Psilocybe cubensis* alcoholic extracts on bacteria (*Staphylococcus aureus* [gram positive], *Escherichia coli* [gram negative]), *Caenorhabditis elegans* (Nematoda), soil microbes (undetermined), and brine shrimp (Arthropoda). Test organisms were introduced to *P. cubensis* extracts and toxic effects were measured after an allotted period of time. In the bacteria bioassay, methanol, *P. cubensis* extracts, and control fungus, *Agaricus bisporus*, extracts had no inhibitory effects with either bacterium at any concentrations tested. Similarly, results of the *C. elegans* bioassay demonstrated low toxicity across all treatments, and no correlation between *P. cubensis* extract concentration and mortality. In the soil microbe bioassay, *P. cubensis* extract exhibited significantly greater antimicrobial properties compared to untreated and methanol controls but did not differ from control fungus extract. In contrast to other bioassays, the brine shrimp bioassay demonstrated the most striking results, with near-universal mortality of all brine shrimp three hours after introduction of *P. cubensis* extract at all concentrations; results not seen in any control treatments, though control fungus extract concentration and mortality were positively correlated. Because *P. cubensis* has demonstrated high toxicity in an arthropod model and insect arthropods share decay niches with psilocybin-producing fungi and contain many fungivores, *P. cubensis* compounds may have evolved, in part, to defend against insects.
Psilocybin production by termite egg-mimicking symbiont, *Fibularhizoctonia* sp.

**Abstract**

Fungi produce neuroactive metabolites that can influence animal behavior and fitness. Due to these effects, some of these metabolites and their synthetic derivatives are used medicinally and possess potential to treat recalcitrant psychiatric conditions, including addiction, depression, and anxiety. However, the ecological roles of these metabolites are poorly understood. Tryptamine-based metabolites are one class of neuroactive compounds that have independently evolved multiple times in Fungi. Multiple tryptamines have affinity to serotonin (5-hydroxytryptamine, 5-HT) receptors. The psychoactive tryptamine psilocybin was first described in the ‘magic mushroom’ genus *Psilocybe*, and primarily agonizes 5-HT₂ receptors. Psilocybin was recently found to be the product of a gene cluster with spotty distribution throughout Agaricales mushrooms, partly due to horizontal gene transfer (HGT). It was speculated that acquisition of the cluster by HGT increased fungal fitness under predation by mycophagous invertebrates. Notably, highly similar homologs of the five Agaricales psilocybin genes were also found unclustered with some gene family expansion in Atheliales. All of the genes were found in the termite symbiont *Fibularhizoctonia* sp. (teleomorph *Athelia*) whereas only psilocybin-associated transporter of unknown function was found in ectomycorrhizal *Piloderma croceum*. Here, we report the production of psilocybin in the sclerotia of *Fibularhizoctonia* sp. using multiple reaction monitoring (MRM) and product ion scan via tandem mass spectrometry. This provides additional evidence of psilocybin production in fungus-insect interactions.
Evolution and genetics of secondary metabolite profiles in ant-farmed coral mushrooms

POSTER A39

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Abstract

Domesticated coral mushroom gardens (family Pterulaceae), farmed by Attine ants of the *Apterostigma pilosum* group, have a distinct evolutionary origin from ant-farmed gilled mushrooms, and convergently coevolved the same interactions with their Attine ant farmers, beneficial bacteria, and parasitic *Escovopsis* mold. Domestication of crops predicts stereotypical genetic changes that confer better crop phenotypes, such as lower toxicity through a loss of secondary metabolite gene clusters. Preliminary comparative genomic data from domesticated and free-living coral mushrooms suggest a reduction in secondary metabolite diversity in one of the coral mushroom cultivars. However, coral mushroom cultivars must still contend with attack from specialist parasitic *Escovopsis* fungi, possibly necessitating the retention of the ability to produce certain defensive compounds. This project will utilize comparative genomics to analyze differences in secondary metabolite-encoding gene clusters in domesticated and free-living Pterulaceae.
Exploring the identity and function of fungal seed endophytes in Coastal Douglas-fir (*Pseudotsuga menziesii* var. *menziesii*)

POSTER A40

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Abstract

Seeds are an essential component of plant life histories, and seed endophytes have the potential to influence germination, seedling establishment and development. That said, seed endophytes are still a new area of study, both in the factors that influence which taxa are present and how these microbes alter plant function. The objectives of this study were to characterize the fungal endophytes present in native and introduced populations of Coastal Douglas-fir (*Pseudotsuga menziesii* var. *menziesii*) seeds, and to test whether some of these endophytes affect seedling drought response. Using culture-based techniques, endophytes were isolated from 8 native populations of Douglas-fir seeds in the United States and 3 introduced populations in New Zealand. Based on the ITS fungal barcode, the dominant taxa present in the sampled seed populations were Trichoderma spp. and Sydowia polyspora. Assessment of endophyte community composition in the United States populations indicates differences based on seed provenance, and future work could further investigate how these communities vary along environmental and plant genetic gradients. To test endophyte function, seedlings from one United States population were inoculated with two isolates of seed-borne Trichoderma spp. and grown under drought conditions. From this experiment, it is expected that inoculated seedlings will have longer survival and improved growth. If the expected results are observed, further study could be conducted on the role of seed endophytes in plant response to abiotic stresses, with applications in mitigating plant stress due to climate change.
Vertical stratification and temporal dynamics of endophytic fungal communities in canopies of Douglas-fir

POSTER A41

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Abstract

Old-growth and late-successional *Pseudotsuga menziesii* play important ecological roles in forests of the U.S Pacific Northwest. These conifers interact with the environment via their canopies, and how these interactions take place can differ within a single canopy along its vertical axis. This work seeks to identify whether canopy characteristics correlate with changes in endophytic fungal community compositions using an Illumina MiSeq metabarcoding approach. Eight trees in the HJ Andrews Experimental Research Forest (Oregon, USA) were climbed and accessible branches were collected along the length of the bole. A single age class of twigs and four age classes of needles were retained from each height. The ITS2 metabarcoding region was amplified directly from needle and twig DNA extractions and sequenced on a 2x300 Illumina MiSeq run. We found that twigs possess more diverse fungal communities than needles, and that the composition of twig and needle communities differed by source tree. Needle and twig communities both vary with vertical canopy position after accounting for source tree, and needle compositions differ according to needle age. Additionally, the relative abundance of *Nothophaeocryptopus gaeumannii*—the dominant endophyte of *P. menziesii* capable of causing Swiss needle cast—significantly affects the relatedness of needle communities across trees. These results suggest that spatiotemporal influence within Douglas-fir canopies is influential in the development of endophytic fungal communities. Determining the extent to which this spatiotemporal influence is due to microenvironmental properties and/or tree ontology requires further exploration.
LIMITED EVIDENCE FOR ECOTYPIC ADAPTATION OF ASCOMYCETES TO DROUGHT

POSTER A42

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Abstract

Communities of animals, plants, and micro-organisms are commonly differentiated along precipitation gradients, yet it remains uncertain whether individuals within species are similarly ecotypically selected, particularly for microbes. To better understand ecotypic adaptations of Ascomycota fungi to environmental conditions, we analyzed stress tolerance for six isolates of for five ascomycete species from sites that experienced up to two-fold differences in mean annual precipitation (MAP) across the central United States. We acquired fungal isolates from Sevilleta National Wildlife Refuge, \textasciitilde 250 mm MAP; Hays Agricultural Research Center, 450-660 mm MAP; and, Konza Prairie Biological Station, \textasciitilde 835 mm MAP. First, utilizing quadrant Petri plates amended with sodium chloride (NaCl) at four concentrations (0–100g/L), we tested the halotolerance of the isolates. Second, we tested xerotolerance using liquid cultures amended with Poly-Ethylene Glycol (PEG) at four concentrations (representing approximate osmotic pressures from -1 to -15MPa). Analyses of estimated NaCl and PEG concentrations that reduced the fungal growth by 50\% (ED\textsubscript{50}) indicated that, although the fungal isolates varied in their halo- and xerotolerances, ecotypic adaptation to prevailing environmental conditions from their site of origin was limited. Our data suggest physiological plasticity in fungal populations adapted to environments with multiple potential stressors. Further experiments using conspecific isolates that vary in environmental tolerances could help to identify the underlying genomic and functional traits of stress tolerance in fungi.
Effect of precipitation, host species, and tissue type on endophytic fungi community composition

POSTER A43

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Abstract

Plant species harbor important microbial symbionts that could help mediate plant response and adaptation to environmental factors. Endophytic Fungi (EF) represent one of the most important plant symbionts. However, processes governing EF community assembly and the effects of ecological context on the evolution of symbiotic interactions remains weakly understood. The objective of this study was to evaluate the effect of precipitation, host species, and tissue type on EF community diversity and richness. We collected leaves and roots samples from *Schizachyrium scoparium* (SCSC) and *Zea mays* (corn) in five locations along a rainfall gradient ranging from eastern South Dakota to south-eastern Minnesota. Fungi were isolated from plant tissues and sequenced using ITS rDNA region primers. EF community will be analyzed to evaluate the relative importance of yearly rainfall, hosts species, and tissue type to EF richness, diversity. We expect that the structure of EF communities will primarily vary with rainfall and geographic distance, and with host identity. Our preliminary results showed that EF colonization does not significantly varies across the rainfall gradient, but rather across host species and tissue types. In addition of their impacts on colonization and diversity, biotic and abiotic factors could have a significant impact on the interaction EF will maintain with their host in varying drought conditions.
Endophyte community shifts in response to drought in monkeyflowers (*Erythranthe laciniata*) grown in native soil.

POSTER A44

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Abstract

All plants have a community of asymptomatic microbes inhabiting their tissue known as endophytes. Increasing evidence suggests that microbes are an extension of plant host phenotype and can ultimately help them adapt in response to stress, including drought (Compant *et al.* 2010). Additionally, stressful conditions may select for distinct endophyte taxa with specific functions (Lemanceau *et al.* 2017). Further understanding of how the structure of endophytes shift in response to drought is a potentially important avenue for identifying significant biotic interactions that may play a role in stress response to climate change and perhaps predicting species distribution shifts. The aim of this project is to examine changes in endophyte communities in plants suffering from drought. We ask, does drought alter microbiome composition, and if so, what part of the plant is changing and are there specific taxa that come into play? We sampled both roots and shoots of *E. laciniata* plants grown in native soil in laboratory 1) controlled and 2) drought conditions. Plant tissues were sampled at two time points in the plant life cycle to account for any shifts over time. All tissue was analyzed for bacterial and fungal taxa. Preliminary results indicate strong differences in endophyte between plant compartments (e.g. roots and shoots), suggesting that root communities are more impacted by the effects of drought than shoot communities. The diversity of endophytes was also greater in the root communities than in the shoot, suggesting transmission of endophytes from their native soil.
Do environmentally adapted fungal communities differ in their tolerance to drought?

POSTER A45

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Abstract

Current environmental change predictions forecast shifts in climatic means, greater climatic variability, and more frequent extremes including floods, droughts and heat waves. It is increasingly evident that plant communities are sensitive to drought and soil-inhabiting microbial communities vary along precipitation gradients. However, the drought sensitivity of the microbial communities remains unclear. Understanding microbial community responses to adverse environmental conditions is vital to elucidating their sensitivity to forecasted changes in precipitation regimes. We sampled soils from an established drought experiment at two sites that vary in their mean annual precipitation (MAP) to assess fungal community responses to naturally existing and experimentally imposed precipitation regimes. We hypothesized that fungal community composition and abundance of drought sensitive taxa would vary in response to MAP and drought treatment. We analyzed our target communities using both culture-dependent and -independent tools to compare the conclusions derived from the two methods. After sequencing communities from environmental DNA and from colony forming units on a drought simulating medium, we estimate that more than 10% of the fungal community and more than 20% of the ascomycetous community was culturable. Our data from the two approaches consistently indicate that while communities were distinct between the two sites differing in MAP, they did not differ between the experimental drought treatments. While recent research indicates that plant and bacterial communities respond to drought, fungal community responses are more elusive, particularly in experiments that impose chronic drought under field conditions.
Drought Stress Leads to Differential Gene Expression in Both Plant and Fungus in Arbuscular Mycorrhizal Symbiosis

POSTER A46

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Abstract

Arbuscular mycorrhizal fungi play an important role in natural and agronomic settings, offering host plants increased uptake of mineral nutrients, pathogen resistance, and abiotic stress tolerance. Improved tolerance to drought stress of colonized plants is well-documented, but the molecular underpinnings of this benefit are poorly understood. To evaluate the impacts of drought on host and fungus, we inoculated carrots (Daucus carota cv. ‘Napoli’) with spores of Rhizophagus irregularis DAOM 197198. Carrots grew in a greenhouse. After carrots established, we imposed water restriction for ten days. Plants were flash frozen, and the fine roots of carrots were used for RNA-seq. Root staining revealed an average colonization percentage of 35% for inoculated plants and no evidence of fungi was found in mock-inoculated controls. Well-watered carrots had significantly higher rates of photosynthetic assimilation, transpiration, and stomatal conductance than those in the drought group, regardless of the inoculation status. Well-watered carrots grew taller shoots and outweighed their drought counterparts (p-value < 0.001). Within the drought treatment, mycorrhizal carrots grew 15% longer shoots than mock-inoculated carrots (p-value < 0.05). There were 12,087 differentially expressed transcripts of carrot and 3,224 for fungus (p-value < 0.05) between well-watered and drought treatments. Preliminary analyses revealed that transcripts associated with fungal aquaporins (AQPs) differed in their response to drought, with AQPF2 upregulated and both AQP1 and AQPF1 downregulated under drought conditions (p-values < 0.001, < 0.001, and < 0.05, respectively). Comparisons of transcriptomic differences between treatments will shed light on the mechanisms leading to improved drought-tolerance of mycorrhized plants.
Soybean Microbiome Under Three Agricultural Management Systems at the Kellogg Biological Station

POSTER A47

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Abstract

Soybean (*Glycine Max*) is a globally significant crop in terms of nutritional and economic metrics. Soybean yields are expected to be at risk as global climate continues to become more erratic in the coming decades. In order to maintain yields, researchers must consider methods that supplement traditional breeding and genetics. One concept that is coming to the forefront in studying plant abiotic stress tolerance is the concept of the plant holobiont.

In order to analyze the microbial component of the soybean holobiont, we performed amplicon sequencing of Fungi, Bacteria, and Oomycete communities associated with soybeans grown under organic, no-till and conventional management systems at Kellogg Biological Station. Sequencing was performed on rhizosphere soil, root, stem, and leaf samples taken at three different time points throughout the growing season. Analysis of Illumina sequencing results revealed significant differences between management systems using PCoA and PERMANOVA analyses in the fungal community associated with soil, but differences were obscured in roots. As expected, soil fungal communities were more diverse across all management systems with between 400 and 600 fungal taxa per sample while the roots contained on average between 150 and 250 taxa per sample. In the no-till management system, root-associated fungal communities were mostly dominated by taxa in *Fusarium* and *Didymella* genera. In the soil, fungal communities were dominated by *Fusarium* and *Mortierella*. Network analysis performed on no-till communities showed several significant hub species with the most highly connected species being the yeast *Sporidiobolus pararoseus*. Efforts to manipulate the soybean microbiome are underway.
Does prairie restoration also restore fungal communities? Examples from two tallgrass prairie sites

POSTER A48

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Abstract

North American tallgrass prairies have been largely converted to row-crop agriculture and maybe only as little as 1% of the historic tallgrass prairies in North America remain intact. Restoration efforts to re-establish prairie vegetation after long-term use in production agriculture is challenging and commonly burdened with questions about what are adequately desirable restoration outcomes. The evaluation of restoration largely relies on analyses of plant communities, whereas it is rarely evaluated whether or not microbial communities resemble those observed in prairie remnants without historic conversion to agriculture. We sampled two prairie sites in eastern Kansas, each with a remnant that had never been converted to row crop agriculture and a post-agricultural site that had been restored. We extracted genomic DNA from roots and leaves of the dominant grass, Schizachyrium scoparium, and MiSeq-analyzed the fungal community richness, diversity, and composition in plants collected from four replicate plots in each of two sites and two land use histories. Our data indicate that the root-associated fungal communities are indistinguishable between the plants from remnants and restored prairies. In contrast, the leaf-associated fungal communities are distinct and those from prairie remnants more diverse than those from restored prairies. While the restoration of the root-associated community composition seems to have been achieved, such outcomes were not obvious in the leaf-associated communities. As a result, we call for greater attention to evaluation of the restoration success of hidden biodiversity.
Native plant responses to mycorrhizal fungi and biochar for ecological restoration of a Pacific Northwest Superfund

POSTER A49

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Abstract

Restoration of highly disturbed ecosystems using mycorrhizal fungi to promote plant growth and survival has been used successfully in a variety of applications. However, there are several barriers that remain challenging for exceptionally degraded sites, such as those impacted by mining operations. Mine soils are typically characterized by low organic material, heavy metal contamination and low pH. The interactions between mycorrhizal fungi and soil amendments, such as biochar have the potential to increase soil pH, immobilize heavy metals while developing a stable store for carbon to promote native plant establishment in former mining sites. Although the possibility of synergism between mycorrhizal fungi and biochar is promising, few studies have tested this within the context of mining restoration. In a greenhouse experiment, I will evaluate the growth responses of two successionally distinct native plant species (*Pseudotsuga menziesii*, *Elymus glaucus*) in contaminated soil from the Formosa mine (Riddle, OR) amended with biochar, mycorrhizal fungi (from local inoculum), or a co-amendment of the two. I hypothesize that amending with biochar and mycorrhizal fungi individually will increase plant biomass compared to un-inoculated controls and that co-amended treatments will synergistically increase plant biomass compared to biochar or mycorrhizal fungi alone. Data on plant growth (e.g., height, leaf number, chlorophyll content) will be collected monthly for six months. Plants will be harvested for biomass and roots assessed for percent colonization by arbuscular and ectomycorrhizal fungi. Results from this study will be used to inform future field studies aimed at improving restoration efforts of abandoned mines.
Next Generation Sequencing analysis of dead wood as a method to study diversity of saproxylic fungi for biodiversity assessment

POSTER A50

Shazneka Blue, Eve Bell, Maria Shumskaya, Christopher Zambell

Kean University, UNION, USA

Abstract

Dead wood is an important component to the conservation of biodiversity in forests. When left to decompose on the forest floor, it protects soil from erosion, promotes nutrient cycling, and provides a unique ecological niche for decomposers such as fungi. The species richness of dead-wood inhabiting fungi can therefore serve as an indicator of the overall health of the forest. Most species of dead-wood inhabiting fungi are cryptic and do not always produce visible fruiting bodies for study. The goal of this project to evaluate new techniques that can be used to quickly assess the diversity of undetectable species present in decomposing wood. Samples of tissue from trees in varying stages of decay were collected near Elizabeth river, NJ and mixed, then DNA was extracted, PCR of ITS gene marker performed and sent for Next Generation Sequencing (NGS). Resulting DNA sequences were analyzed using SCATA pipeline and fungal species or OTU identified based on NCBI database. The results are to demonstrate how many dead wood trunks would require NGS assessment in order to collect information on dead wood fungi representative for the whole location.
Evaluation of Next Generation Sequencing technique as a method to assess saproxylic fungal community composition

POSTER A51

Yassel Hernandez, Julia Annuzzi, Abdurrahim Vardar, Maria Shumskaya, Christopher Zambell
Kean University, Union, USA

Abstract

The focus of our research is to evaluate the potential of Next Generation Sequencing (NGS) method in identification of dead wood fungal species from a specific location, such as an urban park. In North America the research on biodiversity of dead wood fungi is still developing and there is no complete database so far. For our project, 37 fruiting bodies of various dead wood fungi were collected from Ocean County Park during October 2017. The species were identified morphologically where possible, with the conformation by DNA-barcoding. For the barcoding, DNA was isolated from each individual fungal body using DNeasy PowerSoil kit, then amplified by PCR using ITS specific primers to obtain a fragment of ITS gene, which serves as a barcode in fungal identification. This fragment was sequenced, the resulting sequence was compared to the database of fungal ITS sequences in NCBI portal using BLAST and species identified. As a result, a local database of the species found in Ocean County Park was created. NGS sequencing was used as a method allowing metabarcoding of a mixed DNA sample. This method allows to identify species all at once, without individual sequencing. The efficiency and reliability of this method in comparison to the individual species identification is discussed.
Comparative study of microbial community dynamics during wood decomposition in nature

POSTER A52

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Abstract

Despite the important role of saprotrophic fungi in decomposing organic matter and recycling nutrients, the development and diversity of wood decomposing communities remains poorly understood. In a 7-year field experiment in a boreal forest in the midwestern United States, we studied decay dynamics in red pine (Pinus resinosa) and birch (Betula papyrifera) logs using high-throughput sequencing and wood physiochemical analyses (i.e. density loss, ratio of lignin loss relative to density loss, alkali solubility). The effect of bark and decaying position (above- or on-ground contact) in wood decomposition was included in the treatment design. In our previous study, the optimization of environmental DNA extraction from wood samples was performed to obtain high quality DNA for high-throughput sequencing. We hypothesized more brown rot fungal taxa in above-ground wood, with fewer white rot or ectomycorrhizal fungal taxa than ground contact logs, resulting in different decay rate and wood characterization. Faster decay might also occur with bark on, due to high moisture content maintenance. In addition, we hypothesize different bacterial community structures between brown rot and white rot, given brown rot diffuse depolymerization mechanisms and the possible role of bacteria in assisting lignin degradation. Overall, our results, spanning a long-term field experiment and over 600 hundred samples, will provide a comprehensive view of wood decomposing community dynamics and interactions in complex natural ecosystems.
Fungal Succession in a chronosequence of *Populus grandidentata*

POSTER A53

**Buck Castillo¹, Tim James², Chris Gough³, John Syring³**

¹University of Michigan, Ann Arbor, USA. ²VCU, Richmond, USA. ³Linfield, McMinnville, USA

**Abstract**

This study analyzes fungal diversity across varying stages of decay in dead aspen (*Populus grandidentata*) trees in a northern temperate forest. *Populus grandidentata* is a dominant early colonizing tree species in temperate forests across the Midwest since post deforestation due to extensive logging practices in the 19th and 20th centuries. Over the course of the coming decades *P. grandidentata* is beginning to naturally senesce as they are replaced by mid-successional tree species. This is particularly important as coarse woody debris (CWD) is one of the largest precursors to soil organic matter (SOM). Currently CWD contributes only a small portion of the total ecosystem C pool and respiration via the saprotrophs that are actively decomposing the wood. However, as succession in many forests progresses and as disturbances are predicted to increase, the effect of decomposing CWD on ecosystem C fluxes is expected to increase as well. Here we aim to answer two questions: 1) How do trends in fungal community structure differ along a decomposition gradient in *Populus grandidentata*, from standing dead to highly decomposed wood; and 2) how these differences, if any, are related to altered chemistry of the various stages of decomposing *Populus* logs.
Effect of nitrogen fertilization on white- and brown-rot decay of Arabidopsis thaliana litter with variable lignin content

POSTER A54

Allison Gill, Claire Anderson, Sarah Hobbie, Jonathan Schilling
University of Minnesota, Saint Paul, USA

Abstract

Anthropogenic activities such as fossil fuel combustion have increased the availability of reactive nitrogen (N) in terrestrial ecosystems. In many ecosystems, exogenous N addition has been shown to increase soil carbon (C) storage, and this response is sometimes associated with increased retention of lignin-derived compounds within the soil organic matter (SOM) and reductions in the abundance and activity of decomposer fungi in the phylum Basidiomycota. White- and brown-rot wood-degrading fungi within this phylum are important decomposers of lignocellulose, but use distinct metabolic mechanisms (synthesis of class II peroxidases within white-rot fungi vs. oxidative Fenton chemistry within brown-rot fungi) to gain energy from plant tissue. These processes may respond differently to N addition, in ways that depend on the lignin content of the substrate being decomposed. We present results from a laboratory decomposition experiment evaluating the influence of N fertilization on brown- and white-rot decomposition of Arabidopsis thaliana litter with high or low lignin. Decomposer activity of brown rot fungi was suppressed by low-lignin substrates. We also analyzed biomass, extracellular enzyme activity, and CO₂ respiration responses of five fungal taxa with variable metabolic strategies (Gloeophyllum traebum, Postia placenta, Schizophyllum commune, Trametes hirsute, and Pycnoporus cinnabarinus) to N addition treatments. The results provide context for understanding the functional mechanisms by which distinct microbial communities respond to N addition and provides opportunities to understand how these processes may confer changes in SOM composition and chemistry.
Dynamics of microbial groups in response to simulated hurricane at El Yunque Rain Forest in Puerto Rico

POSTER A55

Karleen Gonzalez-Rosario, Sharon A. Cantrell, José R. Pérez-Jiménez

Universidad Ana G. Méndez, Recinto de Gurabo, Gurabo, Puerto Rico

Abstract

Over the past century, the frequency and intensity of hurricanes had increased on the Caribbean; resulting on deforestation and altering natural abiotic conditions. Therefore, it has challenged the stability of forest biogeochemical processes mediated by local microbial communities. Diverse bacteria and fungi driving resiliency and resistance of the forest ecosystem have disassembled by this biological disturbance. Uncovering how bacteria and fungi communities interact with ecosystems drivers under natural disturbances could help elucidate processes to help restore forest conditions. For this, a canopy trimming experiment, that simulated the pass of a hurricane, has been done at Luquillo experimental forest in Puerto Rico. It was designed to understand the effect of canopy opening and debris deposition at forest floor on microbial communities. Our objective is to determine temporal heterogeneity of bacterial and fungi communities in response to detritus deposition of simulated hurricane effect. Two treatments are considered: with and without detritus deposition trimmed from the local canopy. Soil samples were collected from plots, at various times for a period of two years. Total genomic DNA was extracted for the amplification of 16S rDNA and ITS to characterize bacterial and fungal communities using Terminal Restriction Fragment Length Polymorphisms. Bacteria was homogeneous over time for the same plot suggesting microbial succession in which rare microbiota became more prevalent over time. Two-Way PERMANOVA demonstrated significant differences through time and treatment (p=0.99) for the soil fungal and bacterial. Fungal and bacterial communities were heterogeneous among the treatments and through time.
A fungal mechanism to control chaos when deploying oxygen radicals to decay wood

POSTER A56

Claire Anderson, Allison Gill, Jonathan Schilling

University of Minnesota, St. Paul, USA

Abstract

White rot fungi gained the capacity to degrade lignocellulose approximately 295 million years ago when they adapted oxidative enzymes to metabolize lignin. Since then, brown rot fungi have evolved a carbohydrate-selective, two-step mechanism, controlled through differentially expressed genes, that shortcuts lignin removal. In this mechanism, a reactive oxygen species (ROS) system is used to ‘loosen’ plant cell walls followed by the enzymatic hydrolysis of carbohydrates. It is still unclear how brown rot fungi regulate this seemingly ‘chaotic’ ROS system and avoid damaging their own enzymes and hyphae. Specifically, the process that turns ROS pathways on has not yet been identified, despite assumptions of an inducible mechanism. Many studies have suggested that the presence of either lignin or hemicellulose may initiate brown rot decay, but this has not been clearly shown experimentally. I propose to capture the earliest stages of brown rot decay and identify the ROS induction mechanism by using directional fungal growth on wood wafers to track decay progress – creating a space-for-time map of decay along the wafer – and analyzing the whole transcriptome at the incipient stage of decay. I also propose to study how wood components induce the expression of ROS-linked genes and enable brown rot decay by examining decay dynamics and ROS-linked gene expression on modified substrates, such as mutant strains of Arabidopsis thaliana. Understanding the decay mechanisms of brown rot fungi offers potential to harness those pathways for biotechnology applications as well as to make better predictions about the fate of carbon stored in wood.
Soil fungal and bacterial community contributions to wetland carbon storage

POSTER A58

Regina A. Bledsoe, Ariane L. Peralta
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Abstract

Wetlands represent only ~7% of Earth’s surface but contain ~30% of global carbon (C) stores. However, wetland C storage capacity is sensitive to nutrient enrichment from anthropogenic sources such as excess fertilizer use and burning of fossil fuels. Whether a wetland is a C sink or source is primarily driven by rates of fungal and bacterial decomposition of soil organic matter. We can gain insights into mechanisms that determine C storage or loss by understanding how microbial metabolism changes in response to nutrient enrichment. Using a long-term fertilization and disturbance experiment, we examine how nutrient enrichment effects both bacterial and fungal composition and associated soil metabolic profiles. In a previous study, results revealed a distinct shift in bacterial community composition, an increase in bacterial diversity and copiotrophic species, and an increase in soil C in fertilized plots. To investigate how nutrient additions influence fungal and bacterial community composition, metabolic profiles, and microbial plant growth promotion, we compared microbial community structure-function relationships in nutrient enriched vs. ambient plots. We hypothesize a decrease in fungal species and increase in bacterial species diversity and higher metabolic diversity within fertilization treatments. Preliminary results suggest microbial communities from fertilized plots have greater substrate use diversity and faster substrate use rates. Over time, nutrient enrichment of historically low nutrient ecosystems alters C storage potential due to shifts in metabolic diversity of the microbial community. This work will identify substrates and microbial community members to target to further study the mechanisms driving C cycling in wetlands.
DO WOOD-INHABITING FUNGAL COMMUNITIES PREDICT TREE BREAK PATTERNS CAUSED BY HURRICANES?

POSTER A59

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Abstract

Despite their short duration, hurricanes can have strong impact on forests. Hurricane winds can damage trees and subsequently affect forest dynamics and associated ecosystem functions. Climate change is suspected to increase hurricane intensity. In this context, predicting hurricanes damage on trees populations could have a crucial economic importance as well as conservation value. In tropical forests, topography, tree species characteristics (i.e. diameter, growth rate, wood density and biogeographic origin) and tree health have been identified as potential predictors of trees resistance to hurricane. Tree health can be impacted by pathogenic microbes and notably stem wood-inhabiting fungi. Consequently, we speculate that trees infected by pathogenic fungi may be less resistant to hurricane winds by comparison to non-infected trees. To evaluate the potential role of wood-inhabiting fungal communities on the resistance of trees to hurricanes, we sampled logs of nineteen tree species damaged by the hurricane Maria in a Puerto Rican dry tropical forest in 2017. We categorized wood logs depending of two types of hurricane damage; uprooted trees and trees that in which stems were broken. We extracted fungal environmental DNA of logs corresponding to 109 samples. Fungal community composition were assessed using high-throughput DNA metabarcoding. We hypothesize that trees with the snapped stem break pattern will harbor fungal communities enriched in pathogenic fungi relatively to uprooted trees. Finally, we will discuss the utility of microbial communities as disturbance predictor in the light of the emergence of new sequencing technologies.
Characterization of Pathogenic Fungi Associated with Native Species at “El Yunque” National Rain Forest

POSTER A60

Louis F Colon-Santiago¹, Albert Roman-Rivera¹, Nanyrka M. Linares-Alamo¹, Carlos G. Fontanez-Rodriguez¹, Darianne M. Alvarez-Franceschi¹, Sharon A. Cantrell¹, Krista McGuire ², Barbara Roy²

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Abstract

Due to the occurrence of hurricane Maria possible foreign pathogenic fungi could be affecting native tree species. Symptomatology has been observed for leaves, fruits, flowers and seeds, depending on the tree species. We hypothesize the presence of pathogenic fungi are the main cause of the symptomatology. Species studied were Casearia arborea, Prestoea acuminata var. montana, Guarea guidonia and Dacryodes excelsa. For the leaves of Dacryodes excelsa, the symptoms found were the following: small necrotic circular lesion with a yellow halo, irregular lesion, and margin and apex necrosis on leaves. Also, fruits presented necrotic lesions, formation of pycnidia and shield softening. Furthermore, Guarea guidonia presented symptoms like partial necrosis with extended halo, regular and irregular necrotic circular lesions at the margin of the leaf. Seeds and fruits were covered by mycelium. On the other hand, Casearia arborea presented flower necrosis and abortion and Prestoea acuminata var. montana, presented a pink mycelium in seeds collected from the soil. Using microscopy and morphological features, diverse pathogens were found, including: Phoma sp., Phomopsis sp., Pestalotiopsis sp., Colletotrichum sp., Nigrospora sp. and Botryosphaeriaceae family. Thirteen anamorphs were observed to be pathogens. Koch’s postulates were performed to identify the causal agents for the symptoms. Future tests will include DNA extraction and PCR amplification with different gene regions depending on the pathogens to corroborate homology identity. Sequencing will be elaborate with Sanger sequencing method with Big Dye Terminator.
DNA Barcoding and domestication of three *Lentinus* species in Sri Lanka

POSTER A61

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Abstract

The edible wild mushrooms are cultivated and consumed worldwide. In Sri Lanka, only few such species have been accurately identified and domesticated. This study aims the molecular based identification of three edible mushroom species and development of protocols for their experimental domestication. Mushrooms species collected were tentatively identified based on morphological characters of fruiting bodies and culture characteristics in four different media. Genomic DNA were extracted and PCR amplifications of ribosomal Internal Transcribed Spacer (ITS) region were carried out. Initial molecular identification done by NCBI’s BLAST similarity search and phylogenetic analyses confirmed the isolates belong in *Lentinus sajor-caju*, *L. tuber-regium*, and *L. squarrosulus*. Out of rice, corn and corn grits with millet mixture that were tested as mother spawn media, corn showed the highest mycelial colonization density. Out of rubber saw dust (RSD), mango saw dust (MSD) and MSD with corn cobs (CC) mixture that were utilized as growth media, all three species showed the highest colonization rate on MSD. Successful fruiting body formations were observed after 88 and 74 days respectively for *L. sajor-caju* and *L. tuber-regium* on RSD. *Lentinus squarrosulus* produced fruiting bodies on MSD after 49 days. *L. squarrosulus* fructified the most on MSD whereas *L. tuber-regium* showed the highest yields on RSD. All mushrooms tested show the antioxidant properties as assessed by a quantitative Ferric Reducing Antioxidant Power (FRAP) test. This is the first successful domestication effort of *L. sajor-caju* and *L. tuber-regium* in Sri Lanka provided with freshly collected and DNA barcoded strains.
Fungal cannibalism - Assessing fungal decomposition of fungus-based biomaterials

POSTER A62

Molly Moran, Jonathan Schilling
University of Minnesota-Twin Cities, Minneapolis, USA

Abstract

Having the designation of being biodegradable or compostable is a valuable marketing asset, especially given the push for ecofriendly and renewable products. Currently, some companies are utilizing natural organisms, such as fungi, to create more sustainable biobased materials. These materials lack the history of wood and other biomaterial testing, and they reflect novel substrates whose decomposition is of interest in other contexts (example: fungal necromass in carbon cycling). Here, we exposed a fungus-based biomaterial to a range of wood-degrading fungi and quantified various decay parameters, including mass loss, pH, and carbon fractions (lignin insolubles via gravimetric; acid-solubles via HPLC). To do this, we used a block of spent fungal biomass product developed in solid state and placed in a soil block jar with a pre-established hyphal lawn of a known decay fungi for 8 weeks. Nine fungi were tested, including white rot fungi, brown rot fungi, a 'grey rot' fungus (*Schizophyllum commune*), and one soil saprotroph. We found that the greatest mass loss was caused by the brown rot fungi, followed by white rot fungi, similar to rates and patterns typical in wood decay trials with these fungi. The wafer pH and carbon fractions are currently being assessed to track the losses of certain components in the fungal biomaterials, but preliminary acid-insolubles data indicate some disparities within rot types in removal efficiencies/patterns.
Inoculating Media Containing Wood Vinegar Dilutions with Fungi Species

POSTER A63

Christian Marr, Jesse Cerrato
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Abstract

Wood vinegar is a byproduct of wood pyrolysis, a process used to produce biochar, which has significant agricultural value. In its pure state, the wood vinegar is too acidic and concentrated for direct application as agricultural or compost amendments. It does, however, contain a rich diversity and high concentration of valuable organic compounds, which have proven useful and integral in a wide variety of applications (agricultural, industrial, medical, food-related, etc.). Because wood vinegar is generally around 30-40% of the average weight of charcoal/biochar produced during wood pyrolysis, it is valuable to develop more efficient methods of utilizing wood vinegar and making it more directly applicable. Dilutions of wood vinegar produced at Living Web Farms (Mills River, North Carolina) have already shown natural growth of fungi and bacteria species in mostly anaerobic conditions. These naturally occurring "SCOBY (Symbiotic Community of Bacteria and Yeast)-like" cultures were further propagated into media containing various dilutions of wood vinegar (1%, 5%, 20%, and 50%). These same dilutions of media containing wood vinegar were also inoculated with Pleurotus ostreatus, Trametes versicolor, Cordyceps militaris, Ganoderma lucidum, Aspergillus oryzae. Growth rates, metabolic efficiency, pH levels were recorded over a trial period of six weeks. The most successful species with the highest overall growth rates and metabolic efficiency was Aspergillus oryzae. These wood vinegar biological solutions can prospectively be used as an effect inoculant to improve crop vitality, soil health, and compost productivity.
Genomic Identification of Species Sold in Wild Mushroom Food Products

POSTER A64

Bryn Dentinger, Dalley Cutler
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Abstract

Mushrooms have been consumed by humans for many thousands of years. Fruiting bodies can be both aromatically enticing and pleasant to taste, but it has long been recognized that only select species of mushrooms are suitable for consumption. There are adverse health affects of consuming misidentified, inedible mushrooms ranging from mild illness to death. Many food products that have mushrooms as an ingredient use mushrooms that are commercially grown, avoiding these potential health hazards. There are many edible mushrooms that are unable or impractical to be grown commercially yet these mushrooms are still able to be harvested, sold and purchased as food. These products are often sold with the ingredient label of ‘wild mushrooms’, although in some cases the labels do have some level of specificity. For this study we used metagenomic analysis techniques to identify the species of mushrooms that were sold under the label of wild mushrooms in eight different food products. Some of the food products that were sold as porcini and bolete were shown to contain mushrooms that differed from their label, and in some cases the mushrooms present are ones that are not typically considered edible. This study demonstrates a lack of oversight in the labeling of wild collected mushrooms and shows a potential health hazard to consumers.
The activity of *Pleurotus ostreatus* extracts against pathogenic fusaria.

**POSTER A65**

Matias Pasquali, Alessio Scarafoni, Elena Maria Colombo, Chiara Muratore, Francesca Gallotti, Vera Lavelli

University of Milan, Milan, Italy

**Abstract**

A *P. ostreatus* strain, appreciated as food and for the production of nutraceuticals, was grown on a commercial substrate, dried at low temperature (<40°C) and grinded in order to produce a mushroom powder. The bioactivity of the water extract conserved at 4°C in the dark was then assessed on *F. graminearum*, *F. culmorum* and *F. musae* at different time points from production (4 hrs, 40 days, 4 months). Moreover, the effect of the extracts on trichothecene type B production was measured exploiting a *F. graminearum* isolate expressing GFP-tagged trichodiene synthase. This allowed to monitor the first step of toxin production using a microplate fluorimeter.

While mycelial growth of *F. graminearum* and *F. culmorum* was completely blocked at 3 mg/ml, mycelial growth of *F. musae* was inhibited at 90%. MIC50 was measured for *F. graminearum* and *F. culmorum* at 300 micrograms/mL. A loss of the bioactivity of *P. ostreatus* water extract on fungal growth was observed at 40 days (-30%) and of a further -30% at 4 months. A preliminary study on the biological activities of the extract identified a strong protease activity associated to low molecular weight proteins. Their bioactivity decreased over storage time in accordance with a decreased proteolytic activity.

The *P. ostreatus* extract modulates trichothecene production independently from the protease activity, even at concentration where no mycelium inhibition was observed (down to 0.75 micrograms/mL).

Studies on the genetic determinants of the protease activity as well as the compounds able to modulate trichothecene production are ongoing.
Using filamentous Ascomycetes to remove selenium from industrial and municipal wastewaters in Minnesota

POSTER A66

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Abstract

Selenium (Se) is essential in moderate doses to most organisms for the production of selenoproteins, but elevated levels in the environment can cause detrimental biological repercussions. Selenium bioavailability is highly linked to its oxidation state in the environment, and the Se forms common in oxic surface environments are Se(VI) and Se(IV), which are highly water soluble and bioavailable. Current strategies for removing Se from wastewaters are expensive and inefficient, but some environmentally ubiquitous Ascomycetes remove Se from solution by aerobic reduction of dissolved Se(IV/VI) to form solid Se(0) and volatile Se(-II). To this end, culture experiments with Se-reducing fungi, Alternaria alternata and Alternaria strain “F7”, an isolate from Se-contaminated soil, were performed to quantify total Se removed from solution in two Se-contaminated Minnesota wastewaters. In parallel, a second set of cultures were assembled with nutrient-lean culture media (“AY”) and 2000 µg/L or 25 µg/L Se(IV or VI) to reflect the wastewaters’ Se content. In AY, Se(IV) is quickly removed from solution by 7 days and concentrations remain low with time. Conversely, some Se(VI) is removed from solution by 20 days, then concentrations increase to near-initial values, suggesting that Se is recycled back to the media. In the wastewaters, total Se is also removed from solution by 20 days and is recycled back to the media ~8 days later. This experiment provides essential information about fungal mechanisms of Se reduction and information for engineering an efficient aerobic Se bioremediation strategy.
CRISPR-Cas9 Technology as a Tool for Engineering Loss of Heterozygosity Events in *Saccharomyces cerevisiae*

POSTER A67

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Abstract

Mitotic recombination is a universal phenomenon in diploid genotypes. Regardless of being widespread and occurring at a higher rate than mutation, the impact of mitotic recombination on evolution is poorly understood. Previous research has shown that replicate populations of a highly heterozygous genotype of *S. cerevisiae* (cross between a European clinical strain and a wild Chinese strain) grown in a high salt environment have undergone parallel mitotic recombination events. Lines evolved from a heterozygous ancestor with a clinical and wildtype allele frequently become homozygous for the allele derived from the clinical parent, a loss of heterozygosity event. To test the effect of this event, CRISPR-Cas9 technology was utilized to create strains homozygous for the clinical or wildtype allele from the heterozygous strain using allele-specific guide RNAs. Strains homozygous for the clinical allele demonstrated a pronounced difference in growth rate compared to the homozygotes for the Chinese allele, indicating higher fitness in a high salt environment. Genotyping of all engineered strains has shown a variety of genotypes at linked loci, indicating the occurrence of complex crossing over events initiated by CRISPR double-strand DNA breaks. To introduce LOH specifically at a given locus, we are designing a CRISPR multiplexing protocol to create multiple chromosomal double-strand breaks. Multiplexing will be optimized to engineer either single locus or whole arm loss of heterozygosity events. With the development of this technique, it will become possible to study the specific fitness effects of mitotic recombination driven loss of heterozygosity events.
CONSTATX: a tool for improved taxonomic resolution of environmental fungal ITS sequences

POSTER A69

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\textsuperscript{1}Michigan State University, East Lansing, USA. \textsuperscript{2}University of Michigan, Ann Arbor, USA

Abstract

One of the most crucial steps in high-throughput sequence-based microbiome studies is the taxonomic assignment of sequences belonging to operational taxonomic units. Without taxonomic classification, functional and biological information of microbial communities cannot be inferred or interpreted. The internal transcribed spacer (ITS) region of the ribosomal DNA is the conventional marker region for fungal community studies. While bioinformatics pipelines that cluster reads into operational taxonomic units (OTUs) have received much attention in the literature, less attention has been given to the taxonomic classification of these sequences, upon which biological inference is dependent. Here we compare how three common fungal OTU taxonomic assignment tools (RDP Classifier, UTAX, and SINTAX) handle ITS fungal sequence data. The classification power, defined as the proportion of assigned OTUs at a given taxonomic rank, varied among the classifiers. Classifiers were generally consistent (assignment of the same taxonomy to a given operational taxonomic unit) across datasets and ranks; a small number of OTUs were assigned unique classifications across programs. We developed CONSTAX (CONsensus TAXonomy), a Python tool that compares taxonomic classifications of the three programs and merges them into an improved consensus taxonomy. This tool also produces summary classification outputs that are useful for downstream analyses. Our results demonstrate that independent taxonomy assignment tools classify unique members of the fungal community, and greater classification power is realized by generating consensus taxonomy of available classifiers with CONSTAX.
Reflections from the identification of a new class-level lineage: A few methodological considerations to help enable the connection of unidentified environmental DNA sequences to the unknown fungi they represent

POSTER A70

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Abstract

Only a small percentage of the world’s fungi is currently described, and the large amount of unidentified fungal sequences detected through environmental DNA sampling is a significant complication for community studies that rely on metabarcoding techniques. Many sequences detected in such studies represent fungi that a) are widely distributed (detected frequently across independent studies from around the world), b) are highly abundant (as inferred by sequence read abundance), or c) belong to unknown, deeply-diverged lineages. One group of sequences that fits all of these descriptions belongs to Archaeorhizomycetes, a class estimated to contain hundreds of species, but for which few pure-culture representatives exist. Utilization of resources and data generated during investigations into the diversity of this class, coupled with the identification and phylogenetic placement of multiple unidentified class- and order-level lineages revealed in a separate unrelated study, has now led to the connection of living fungal representatives to a different unidentified class-level lineage. Progress toward formal description and inference of ecological traits for this new lineage will be presented. Characteristics of each study that made this connection possible and aspects of OTU clustering methods that hinder essential cross-study comparison will also be discussed. A set of practices is proposed to facilitate future connections between unidentified environmental DNA sequences and their living fungal counterparts. If widely adopted by the research community, these practices could potentially help alleviate some of the issues arising from unidentified DNA sequences in reference databases and contribute toward a more complete understanding of fungal diversity.
Integrating the North American Mycoflora Project in an Introductory Biology Course.

POSTER A71

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Abstract

Recent efforts by the North American Mycoflora Project (NAMP) to recruit and engage citizen scientists (Mycoflora 2.0) are helping to advance the goal to identify and map the distributions of macrofungi in North America. An educational product was piloted in a college-level Introduction to Biology Laboratory course where microscopy, PCR, and bioinformatics are taught to evaluate the potential of NAMP as an instructional instrument. Three of four lab instructors and 120 of 180 students participated. Forty-eight voucher specimens from the VSC Herbarium’s Fungus Collection, one per student group, were processed. Each group received a bag with a split duplicate from the collection, a spore print when available, and the taxonomic name. Students used microscopy and a handout with spore terminology to write a description of the spores, and compared their description to those published in mushroom keys. Students also collected a tissue sample for NAMP sequencing. The time between tissue collection and the bioinformatics lab was sufficient to receive the sequence results. Sequence success rates and voucher accuracy data will be presented, as will reflections from instructors. Assessments of student knowledge will also be discussed. An educational product of this sort would allow NAMP to access lab fees as a funding source, and perhaps attract young scientists to the field. The donation of high quality materials from NAMP participants, such as well preserved duplicates and extra spore prints, in exchange for reduced sequencing costs, is one way this product could be scaled-up.
The Mycological Society of America Student Section

POSTER A72

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Abstract

The Mycological Society of America Student Section is a student-run group within MSA, which aims to (1) facilitate communication among all students of the Society, (2) provide opportunities for students to network with other individuals in their own research fields and beyond, and (3) connect student members of MSA with scientists performing cutting edge mycological research. Thus, the Student Section has the potential to inspire future collaborations. For this year’s annual meeting in Minneapolis, MN, the Student Section organized the symposium “O the places you’ll go: Career opportunities in mycology,” to discuss the breadth of mycological careers available. The speakers will address the challenges and opportunities of their careers, and how training in mycology led them to their current positions. This symposium provided an excellent opportunity for exposing attendees of the meeting to a diversity of careers outside of the traditional academic realm. The Student Section is open and inclusive, welcoming the participation of graduate students, postdoctoral researchers, and faculty in this group. We hope you can join us at our future events!
Tar Spot of Corn: Distinguishing the fungal communities of tar spot and fish-eye symptoms through amplicon sequencing

POSTER A73

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Abstract

Tar spot is a fungal disease complex of corn that has been destructive and yield limiting in Central and South America for nearly 50 years. *Phyllachora maydis*, the causal agent of tar spot, is an emerging corn pathogen in the United States. The tar spot disease complex putatively includes *Monographella maydis* (syn. *Microdochium maydis*), which increases disease damage through the development of necrotic halos surrounding tar spot lesions. These necrotic halos, termed “fish-eye” symptoms, have been identified in the United States, though *Monographella maydis* has not yet been confirmed. In this study, next-generation sequencing of the internal transcribed spacer-1 (ITS1) ribosomal DNA was used to identify fungal taxa that distinguish tar spot infections with or without fish-eye symptoms. Fungal communities within tar spot only lesions were significantly different from communities within fish-eye lesions. Interestingly, a single OTU was found to be significantly more abundant in fish-eye lesions compared to tar spot lesions and had a 91% ITS1 identity to *Neottiosporina paspali*. In addition, this OTU was positively associated with fish-eye symptom networks, but not in tar spot symptom networks. Many OTUs identified as *Phyllachora maydis*, suggesting that different isolate genotypes may be capable of causing both tar spot and fish-eye symptoms, independent of other fungi. We conclude that *Monographella maydis* is not required for fish-eye symptoms in tar spot of corn.
Bringing fungal virology out of the dark ages of sequencing

POSTER A74

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Abstract

Viruses are universal symbionts that have undoubtedly shaped evolution. Progress in understanding the impact of viruses on fungal evolution, however, has been paralyzed by a lack of sampling and a lack of sequencing methodology. Here, we compare methods developed for the next-generation sequencing of double-stranded RNA mycovirus genomes on three platforms: Pacbio, Illumina, and Oxford Nanopore. Further, we use these methods to sequence the viromes of 30 individuals from early-diverging fungal lineages. With this greatly improved representation of mycoviral sampling across Fungi, we will test the hypothesis of fungus/virus cospeciation. This project brings mycoviruses into the modern era of sequencing and expands our knowledge of mycoviral breadth and diversity.
Identification of unknown fungus susceptible to fungicide in *Glycine max* roots

**POSTER A75**

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**Abstract**

Soybean production in modern agriculture is challenged by availability of suitable land, water, increase in number of pathogens and excessive dependence in the use of agrochemicals. Fungal symbioses with plants are key in the acquisition of nutrients from soils and plant health. However, our understanding of the effects of excessive use of fungicides on fungal communities is limited. We compared fungal communities associated with soybean roots before and after fungicide application using Illumina sequencing. A dominant unknown fungus significantly decreased in abundance after fungicide application. The objective of this project was to characterize this unknown fungus using molecular methods. The unknown fungal species (Operational Taxonomic Unit 44) decreased 35% after fungicide application and it was not possible to identify using Blast searches in Genbank. Specific primers in the ITS rDNA region were designed using Primer 3 Plus Software. The primers were tested using polymerase chain reaction (PCR) on environmental DNA soybean samples to compare pre and post-fungicide roots. In addition, longer sequence fragments from soybean leaf and root DNA were obtained using the new primers in combination with fungal specific primers for the ITS and LSU region. Preliminary results indicate OTU44 belongs to a group of dark septate fungi in the order Pleosporales, which are commonly overlooked in environmental studies. Future work will focus on culturing soybean root material to isolate OTU44.
Identification of Mitogen-Activated Protein Kinase (MAPK) genes in *Alternaria oxytropis*

POSTER A76

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Abstract

The signaling cascades of Mitogen-activated protein kinase (MAPK) play a key role in the transduction of downstream signals in all eukaryotes. The presence of MAPK genes and their signaling mechanisms are not well understood in endophytic fungi. MAPKs have been implicated in pathogenicity, secondary metabolism, and conidiation. *Alternaria* contains several species that adversely affect crop production and produce mycotoxins that are harmful to plants and animals. The fungus *Alternaria oxytropis* is prevalent in western North America and China in arctic and alpine regions as an endophyte within *Oxytropis* sp. plants. The fungus produces the toxin swainsonine, the consumption of which causes locoism in cattle. Among the MAPK pathways categorized in *Alternaria*, Fus3, Hog1, and Slt2 mediate signaling cascades that play a significant role in conidia formation, pathogenicity, and osmotic stress.

Using high-throughput sequencing and genome analysis, we identified Fus3, Hog1 and Slt2-type MAPK genes from *Alternaria oxytropis* that were 86.73, 88.19, and 87.66 % identical, respectively, to those from *Alternaria alternata* in the NCBI database. Using primer design and PCR, we were able to verify the presence of these MAPK genes in *Alternaria oxytropis*. Phylogenetic analysis of MAPK genes from genomes of 11 fungal species from 4 orders and 2 phyla reveal that MAP Kinases are highly conserved in several species of the genus *Alternaria* and order Pleosporales. Analysis of gene transfer events of MAPK genes and proteins in *Alternaria* should provide more details about their biological functions.
Genome analysis of *Neonectria* species associated with beech bark disease

**POSTER A77**

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**Abstract**

Beech bark disease (BBD) of American beech (*Fagus grandifolia*) was first recorded in the United States in 1930 and since then has steadily spread throughout the host’s native range. The disease in North America progresses in stages with the first involving damage to the outer bark by the invasive scale insect *Cryptiococcus fagisuga*, followed by infection of *Neonectria ditissima* or *N. faginata*. In this study, the genomes of *Neonectria faginata* M1600 (*F. grandifolia*, North America), *N. ditissima* CBS 226.31 (*F. sylvatica, Germany*) and *N. coccinea* CBS 119158 (*Fagus* sp., Germany) were sequenced using Illumina technology and compared to related bark pathogens *Corinectria fuckeliana* CBS 125109 (*Pinus* sp., NZ) and *N. punicea* CBS 134248 (*Castanea* sp., France). The estimated genome sizes after de novo assembly for the beech bark pathogens were as follows: *N. faginata*, 42.0 Mb (1,349 contigs, N50 94,700 bp); *N. ditissima*, 42.2 Mb (1,367 contigs, N50 87,448); and *N. coccinea*, 41.3 Mb (997 contigs, N50 108,701). The estimated genome size for *C. fuckeliana* was 40.0 Mb (1,522 contigs, N50 121,868 bp), while for *N. punicea* it was much larger at 55.2 Mb (3,561 contigs, N50 38,224). Using AUGUSTUS, 13,137 protein-coding genes were predicted for *N. faginata*, 13,482 for *N. ditissima*, and 12,857 for *N. coccinea*. The predicted number of protein-coding genes for *C. fuckeliana* was 11,462, while *N. punicea* had 21,376 predicted protein-coding genes. As expected given the close relationship, *N. faginata* shared more genes clusters *N. coccinea* than with the more distant *N. ditissima*. 
Mutations altering transport function result in decreased virulence and DON accumulation in *Fusarium graminearum*

POSTER A78

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Abstract

The plant-pathogenic fungus *Fusarium graminearum* causes Fusarium Head Blight (FHB) disease of small-grain cereals. FHB causes necrosis and contaminates grains with potent mycotoxins. Some mycotoxins are required for virulence to plants and cause large economic losses annually. Control of FHB and mycotoxin contamination of grain is difficult with current methods and so we wish to understand how *F. graminearum* delivers its toxins to plants in order to reduce their accumulation and resulting harmful effects. We have focused on mycotoxin export via ATP Binding Cassette (ABC) and Major Facilitator Superfamily (MFS) transporters, as well as exocytosis-mediated export. Single deletion mutants for numerous ABC and MFS transporters showed reduced mycotoxin accumulation *in vitro* and *in planta* and reduced virulence. Similar results were found for a deletion mutant in a gene essential for an exocytosis-related pathway. To determine if functional redundancy occurs in these export systems, multiple mutations were introduced into a single strain. Certain mutation combinations resulted in additive effects or potentially synergistic effects in reducing mycotoxin accumulation and virulence. Disrupting multiple mycotoxin export mechanisms simultaneously can nearly eliminate mycotoxin accumulation and virulence *in planta*. These results may be helpful in providing targets for designing new, more effective, management strategies for FHB.
Polyol transporters from the lichenizing fungus *Peltigera britannica*

**POSTER A79**

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**Abstract**

Lichenizing fungi subsist on carbon provided by their photosynthetic symbionts. Carbon is transferred to the lichenizing fungus as glucose when the primary photobiont is a cyanobacterium, and when the primary photobiont is a green alga, carbon is transferred as the polyol ribitol. Although the nature of the carbon source is well known, the proteins that facilitate symbiotic carbon exchange are not. Glucose transporters have been extensively characterized in many organisms, but transporters capable of carrying polyols such sorbitol, xylitol, arabinol, and ribitol are comparatively less studied, particularly in the lichen symbiosis. To identify and characterize the transporters responsible for translocating carbon from the green algal photobiont to the mycobiont in the lichenizing fungus *Peltigera britannica*, DNA sequences from five functionally characterized polyol transporters from the yeast *Debaryomyces hansenii* were used. Degenerate primers were developed, and genes encoding two putative polyol transporters capable of transporting ribitol were amplified from DNA extracted from *P. britannica* thalli. A full-length cDNA sequence codon-corrected for expression in *Xenopus* oocytes was subcloned into a *Xenopus* oocyte expression plasmid. From this plasmid, cRNA was produced and injected into *Xenopus* oocytes. The functionality of the transporters was tested by electrophysiology.
Analyzing the *Phytophthora* pathogen on tree tomato (*Solanum betaceum*) in Ecuador

**POSTER A80**

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**Abstract**

Tree tomato (*Solanum betaceum*) is native to the Andean region in South America and an export crop in Ecuador. Interestingly, two different *Phytophthora* species have been found to cause blight disease on tree tomato, *P. andina* in Ecuador and Peru, and *P. betacei* in Colombia. Recent studies describe the pathogen populations in Peru and Colombia, while the Ecuadorian population has not been reviewed in over a decade, after *P. andina* was first described. We obtained 154 isolates of *P. andina* from tree tomato from 20 localities along the Ecuadorian highlands. Mating type of all Ecuadorian samples tested was A1, versus the A2 mating type reported in Peru. Morphological analyses showed differences in the length-to-breath ratio of sporangia, being smaller in the current *P. andina* Ecuadorian population (2.05) compared to the older population (2.4-2.7), and to *P. betacei* (2.6). The presence of hyphal swellings was recorded for the first time in North-eastern Ecuador. Recent *P. andina* samples were able to grow and sporulate on PDA media, as opposed to *P. betacei*. Mitochondrial haplotypes were the same for past and current Ecuadorian *P. andina* samples and *P. betacei* (Ia), but different from Peru (Ic). Sequence at the COXII locus was the same between present and past *P. andina* Ecuadorian samples and different from *P. betacei*. Our results indicate no major changes in the *P. andina* population on tree tomato in Ecuador in the past decade, but corroborate differences with *P. betacei* from Colombia and *P. andina* from Peru. Genetic analyses are ongoing.
Sorghum mycobiome: Stochasticity, succession and partner selection.

POSTER A81

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Abstract

Community assembly of fungi associated with crops is thought to be strongly influenced by the deterministic selection of host plants, rather than stochastic processes. Here we use a simple, sorghum [Sorghum bicolor (L.) Moench] system with abundant sampling to discover that a completely stochastic force, ecological drift, acts in leaves and roots early in host development, when the mycobiome is small, and again when sorghum is stressed by drought. For all fungi, host compartment exerted the strongest effects on mycobiome assembly, followed by the timing of plant development and lastly by plant genotype. For arbuscular mycorrhizal fungi, alone, host plant development exerted strongest effect on community assembly, followed by compartment and lastly by plant genotype. We now are analyzing the plant transcriptome to investigate the host plant’s role in AMF partner selection and succession.
The genome of *Gloeostereum incarnatum*, provides insights into the genetic basis of its medicinal properties

**POSTER B2**

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**Abstract**

Abstract: *Gloeostereum incarnatum* is an edible mushroom that is widely grown in Asia countries. Several studies have suggested that *G. incarnatum* possesses antioxidant, immunomodulatory, anti-inflammatory, anti-proliferative, and antibacterial properties, though their genetic basis are still unknown. In this study, we present a high-quality genome of *G. incarnatum* using the single-molecule real-time (SMRT) sequencing platform. Our *G. incarnatum* genome assembly was 38.67 Mbp, with an N50 of 3.5 Mbp, encoding 15,251 proteins. Phylogenetic divergence date analysis estimated that the *Cyphellaceae* diverged ~174 million years ago from other fungi. The *G. incarnatum* genome encodes multiple genes and gene clusters in association with lignocellulose degradation, secondary metabolites, and polysaccharide biosynthesis. Particularly, we identified two terpenoid-associated gene clusters. Both contain a gene encoding a sesterterpenoid synthase and are adjacent to a gene encoding a cytochrome P450 enzyme. These gene clusters are likely to participate in the biosynthesis of incarnal, which is a known bioactive sesterterpenoid produced by *G. incarnatum*. This study provides insights into the genetic basis of *G. incarnatum*’s medicinal properties, and serves as a first step towards the applications of bioactive proteins produced by this fungus for pharmaceutical uses.
Acrophiarin (antibiotic S31794/F-1) from *Penicillium arenicola* shares biosynthetic features with both *Aspergillus*- and *Leotiomycete*-type echinocandins

**POSTER B3**

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**Abstract**

Echinocandins are first-line therapies for invasive fungal infections due to their efficacy and safety. Based on phylogenetic inferences and chemical structures, echinocandins have been classified into two types, *Aspergillus* (Eurotiales)-type, e.g., echinocandin B, and *Leotiomycete*-types, e.g., pneumocandins. Acrophiarin is an echinocandin with a peptide core bearing hydroxy-glutamine like that of the pneumocandins, but with a myristoyl side chain, presumably originating from cellular fatty acids, rather than the dimethyl-myristoyl side chain, biosynthesized by a polyketide synthase as in the pneumocandins.

Acrophiarin (synonym antibiotic S31794/F-1) is produced by *Penicillium arenicola* (Trichocomaceae), a species phylogenetically distinct from echinocandin-producing *Aspergillus* species of the Trichocomaceae. Recent phylogenetic studies indicate that *P. arenicola* should be transferred the genus *Phialomyces* (Trichocomaceae). To understand the evolutionary steps leading to the diversification of the echinocandin lipopeptides, we have produced acrophiarin from the original strain NRRL 8095 from British Columbia soil. The genome of NRRL 8095 was sequenced, and the acrophiarin biosynthetic gene cluster was identified. We integrate the acrophiarin gene cluster into a revised evolutionary framework, show that its biosynthetic and transport genes bridge the gap between the two echinocandin types, and provide evidence of horizontal gene transfer during the evolution of the echinocandins. Furthermore, acrophiarin and its analogues are characterized with new spectral and antifungal data. We demonstrate that acrophiarin is a chemotaxonomic marker for *P. arenicola*. Hence, the full recognition of the range biosynthetic variants among echinocandins will provide options to generate and identify new echinocandins and to design experiments to understand their natural functions.
Global regulators VeA, LaeA and McrA govern secondary metabolism and morphological development in the echinocandin-producing fungus *Aspergillus pachycristatus*

POSTER B4

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Abstract

Fungi produce a wide range of secondary metabolites (SMs) and bioactive compounds with potential biotechnological value and significant ecological functions. The biosynthetic genes for secondary metabolites are usually located in clusters, with or without a pathway-specific regulator. In addition to pathway-specific regulation, global regulation plays an important role in coordinating fungal development and secondary metabolism.

*Aspergillus pachycristatus* is a sister species of the model organism *A. nidulans*. Comparisons of the genome of *A. pachycristatus* NRRL 11440 with *A. nidulans* FGSC 4A predicted the two species share approximately 40 SM gene clusters but are divergent in about 10-15 gene clusters including those for penicillin and echinocandins. To investigate how global regulators influence the expression of SMs and culture morphology in *A. pachycristatus*, we generated gene disruption mutants of *veA* and *laeA* (velvet complex) and *mcrA* (master transcription regulator). Untargeted MS-based metabolomics was used to compare and quantify the changes in expression of SMs. The *veA* disruption caused about 18 metabolites to increase >6-fold in their relative levels, including triacetylfusarinine and its analogues that have >100-fold increases, while about 12 metabolites decreased >5-fold. Overall decreases in metabolites were characteristic of the *laeA* mutant, while increases of most metabolites occurred in the *mcrA* mutant. As predicted from the genome sequence, we report for the first time that *A. pachycristatus* produces many of the same SMs as *A. nidulans* including felluatmides, emericellamides, aspernidine, aspercryptin and others, from known and unknown biosynthetic pathways.
Expanding the molecular detection toolkit for *Coccidioides* by documenting genetic variation from patients treated in New Mexico and testing environmental samples

**POSTER B5**

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**Abstract**

Coccidioidomycosis is caused by species of *Coccidioides* that infect humans and animals when arthrospores are inhaled. It often presents as a lung infection that can evolve into pneumonia or a systemic infection. While progress has been made in understanding the risk factors for hosts and the biology of infection, the environmental conditions that influence the distribution of these fungi remain elusive, rendering it impossible to predict the potential for range expansion, emergence of new pathogenic lineages, or increase in incidence with changes in environment or climate. We recently conducted the first analysis of *Coccidioides* clinical isolates from New Mexico. While New Mexico is in the coccidioidomycosis endemic zone and was predicted to have *C. posadasii*, our results indicate that both *C. immitis* and *C. posadasii* were present among these isolates. Five of eight infections for which patient ethnicity was known occurred in Native Americans, suggesting a need for studies to determine if American Indians represent a risk group. More broadly, we are targeting regions of mtDNA to 1) improve detection of low levels of *Coccidioides* sequences in environmental samples and tissues, and 2) to improve our ability to distinguish between the two species rapidly. While approaches using real-time PCR have shown success, results with environmental samples have been patchy, and current methods lack species specificity. We would also like to expand detection methods to include other medically-important members of the Onygenales. These molecular approaches have potential to advance disease ecology studies and to aid in accurate, timely, and cost-effective diagnosis.
An Ex Vivo Corneal Culture Model to Assess Antifungal Sensitivity of Fungal Species Associated with Equine Fungal Keratitis

POSTER B6

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Abstract

Equine Fungal Keratitis (EFK) is a severe, progressive inflammatory eye disease due to invasive growth of fungi into the cornea, and may result in blindness. Cullen et al. (PLOS ONE 2019) recently determined that *Aspergillus flavus*, *A. fumigatus*, and *Fusarium falciforme* represented the fungi most commonly isolated from EFK from the Southeastern United States, based on morphological characterization and multi-locus DNA sequence analysis. Fungal species sampled from EFK also exhibited differences in minimum inhibitory concentration (MIC) antifungal agent susceptibility using in vitro based assays. In this study, antifungal drug sensitivity using the in vivo wax moth larvae (*Galleria mellonella*) and excised (ex vivo) porcine corneal culture models were compared. Relative in vitro antifungal drug sensitivity did not consistently correlate to the in vivo response observed in the *Galleria* model. In general, corneas incubated in drug-infused DMEM medium were inhibited at concentrations similar to those seen in vitro, but antifungal drugs with known poor corneal penetration required concentrations above MIC to completely inhibit growth within the cornea. Results using the *Galleria* model system to assess antifungal drug sensitivity were variable and differed from the ex vivo corneal system. These experiments support the value of the in vitro system for providing baseline sensitivity data and of the ex vivo corneal model for more closely approximating EFK and its response to antifungal drugs. Both the in vitro and ex vivo models are being used to identify potential new therapeutic agents for EFK.
Predicting species boundaries and biodiversity in the genus *Pneumocystis*

**POSTER B7**

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**Abstract**

The genus *Pneumocystis* exemplifies a crisis in mycology: far more biodiversity exists in the kingdom Fungi than we have described, or could describe in several lifetimes at current rates of species discovery. Fungi in this genus live exclusively in the lungs of mammals and have been detected in every mammal species tested. Patterns of coevolution with mammalian hosts and demonstrated host specificity suggest that thousands of *Pneumocystis* species may exist, potentially equal to the number of mammal species. However, only five species have been described, with no new species descriptions published since 2006. Meanwhile, hundreds of *Pneumocystis* genetic sequences have been collected from a variety of hosts without being formally identified. Here, we discuss the causes of this failure to describe species hiding in plain sight, and we call researchers to action in this endeavor. We also identify potential undescribed *Pneumocystis* species using genetic species delimitation techniques. Results support the existence of many more *Pneumocystis* species than are currently known, but several are apparently capable of infecting many closely-related mammals (i.e. those in the same genus). Additionally, we predict that there may be 3,000 to 5,000 *Pneumocystis* species inhabiting the 6,399 currently recognized mammal species. Although crude, our prediction challenges the dominant perspective of strict specificity between mammals and *Pneumocystis.*
The Genus *Hebeloma* in the Rocky Mountain Alpine Zone

**POSTER B8**

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**Abstract**

Numerous taxa of *Hebeloma* have been reported in association with *Salix*, *Dryas*, and *Betula* in arctic-alpine habitats. However, species are notoriously difficult to delineate because morphological features overlap, and previously there was little reliable molecular data available. Recent progress in ITS-sequencing within the genus, coupled with an extensive database of parametrically described collections, now allows comparisons between species and their distributions. Here we report 16 species of *Hebeloma* from the Rocky Mountain alpine zone from some of the lowest latitudes (latitude 36°–45°N) and highest elevations (3000–4000 m) for arctic-alpine fungi in the northern hemisphere. Twelve of these species have been reported from arctic-alpine habitats in Europe and Greenland and are now molecularly confirmed from the Middle and Southern Rockies, greatly expanding their distribution. These are: *Hebeloma alpinum*, *H. aurantioumbrinum*, *H. dunense*, *H. hiemale*, *H. marginatulum*, *H. mesophaeum*, *H. nigellum*, *H. oreophilum*, *H. subconcolor*, *H. spetsbergense*, *H. vaccinum* and *H. velutipes*. *Hebeloma hygrophilum* is known from subalpine habitats in Europe, but was never recorded in arctic-alpine ecology. Three species recorded from the Rockies, but as yet not reported from Europe are *H. alpinicola*, *H. avellaneum* and *H. excedens*. The last two have never previously been reported from an arctic-alpine habitat. For all three of these species, the holotypes have been studied, morphologically and molecularly, and have been incorporated into the analysis.
Species discovery among British Columbia’s fibre cap mushrooms through a phylogenetic analysis of the Inocybe “praetervisa” group

POSTER B9

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Abstract

*Inocybe* section *Marginatae* includes difficult species complexes and many as-yet undescribed species. In British Columbia, Canada, specimens identified under as three different species representing the *Inocybe praetervisa* clade in Sect. *Marginatae* have been collected repeatedly. Although the *I. praetervisa* clade is better studied than many other groups, knowledge about its species diversity still has gaps. This became evident when analysis of the DNA sequences of the ITS and RPB2 region showed that BC specimens were divided into three well-supported clades, provisionally named species 4, 5, and 7, all of which differed from published species of the *I. praetervisa* clade. 'Species 4' was represented by 6 collections which consistently formed their own clade concluding it to be a novel species. Species 5 consistently formed its own clade but represented by only three samples from one locality, within-species variation could not be assessed. Species 7 was distributed with *I. salicis-herbaceae* and *I. phaeocystidiosa*. Research from this study demonstrates the difficulty of morphological species identification because of the overlap of morphological characteristics. It highlights the utility of molecular analysis of both ITS and RPB2 regions for further studies on the *Inocybe praetervisa* clade.
A bird in the nest is worth how many in the family? Systematics and evolution of the bird’s nest fungi (Nidulariaceae, Agaricales)

POSTER B10

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Abstract

Bird’s nest fungi (Nidulariaceae) are a diverse, morphologically distinctive, and globally distributed group of saprotrophic fungi. Studies show that Nidulariaceae species are potential sources of medicines, but the systematics and evolution of these fungi are vastly unexplored. The majority of bird’s nest fungi (Cyathus, Crucibulum, and Nidula) have open, cup-shaped basidiocarps whereas Nidularia and Mycocalia have closed globular basidiocarps that break apart at maturity. It has been hypothesized that taxa with closed basidiocarps represent the ancestral state of this group. Several studies have addressed the systematics of bird’s nest fungi but have focused exclusively on Cyathus. A six-gene phylogeny of Agaricales placed bird’s nest fungi sister to Cystoderma (Agaricaeae). However, the taxon sampling was not representative of either Cystoderma or Nidulariaceae and the relationship was not highly supported. We conducted a phylogenetic analysis using ITS, 28S, and RPB2 regions from diverse bird’s nest fungi. Our results indicate that bird’s nest fungi are divided into two distinct clades: the /cyathus lineage and the /mycocalia-crucibulum-nidula-nidularia (MCNN) lineage. Cyathus and Crucibulumare are strongly supported as monophyletic groups, whereas Nidula and Nidulariariae are not. Crucibulum laeve represents a species complex with several geographical subclades. Taxa with enclosed basidiocarps were recovered in multiple distant lineages in our analysis, suggesting that there have been several transitions of basidiocarp morphology over time. More samples of Mycocalia are needed to reconstruct the ancestral state and determine the placement of Mycocalia within the family. Relationships between bird’s nest fungi and other Agaricales members are also discussed.
Uncovering the True Diversity of Chanterelles in Indiana

POSTER B11

Jairus Chittenden, Stephen Russell
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Abstract

Chanterelles are some of the most popular wild mushrooms in Indiana and throughout the Midwest. These attractive orange and yellow fungi are a natural delicacy, and the global trade in chanterelles exceeds $1 billion per year. Like so many other clades of fungi, only a fraction of the chanterelles’ true diversity in North America is known to science. Given their economic and ecological value, chanterelles deserve a phylogenetic analysis using the full capabilities of modern DNA sequencing technology. This project will determine how many species of chanterelles there are within Indiana and how they are related to each other and species across the world. DNA was extracted from over 100 chanterelle specimens collected during the recent Indiana Mycoflora Project, and the genes for transcription elongation factor 1 (TEF1) and the large ribosomal subunit (LSU) were used as barcode regions. Incorporating observations of each specimen’s morphology, the sequence data were compared with previous database entries and published literature on Midwestern chanterelles. At least 11 known species have been identified in Indiana, as well as five candidates for species new to science. The discovery of new species and unexpected diversity will generate public interest in mycology from mushroom hunters throughout the state and beyond.
Shiitake and its relatives, progress on 30 new genomes in the genus *Lentinula*

**POSTER B12**

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**Abstract**

*Lentinula* is a genus of “white rot” wood decay fungi found on hardwood trees across Asia, Oceania, and in tropical and subtropical regions of North and South America. Including the most cultivated mushroom globally, shiitake, the genus contains at least six morpho-species. In the first global sampling and genome sequencing effort for this genus we collected and sequenced 30 isolates spanning all described species and the known geographic distribution. Genomes range in size from 35.6 Mbp to 49 Mbp, arranged in 67-2000 contigs, with between 12,000 estimated genes in the shorter genomes and 16,000 estimated genes in the longer. Phylogenies based on the ribosomal spacer ITS, divide the genus reliably into “New World” and “Old World” clades covering Australasian and American isolates respectively. However, species level resolution has long remained fluid, with a number of divisions within established species. Here we present the current status of the project and our growing understanding of the genus. We will present new and more robust phylogenies of the genus created utilizing an array of single-copy genes as well as single nucleotide polymorphism (SNP) profiles. The inclusion of wild and cultivated strains within the dataset has also allowed for clustering analysis and exploration into gene copy number variations associated with a history of domestication. These analyses move towards a better resolution of the species level diversity of the genus, expand on our knowledge of its divergence and history, and open up other aspects like substrate adaptation for investigation.
Colorado Tulostoma: Towards a global phylogeny

POSTER B13

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Abstract

Tulostoma Pers. is a cosmopolitan genus of stalked puffballs in the family Agaricaceae. Tulostoma species diversity is greatest in arid and semiarid areas, but some species occur in areas which receive greater precipitation. Spore morphology in this genus ranges from smooth to strongly and variously ornamented. It has been proposed that in this genus spore ornamentation increases with available moisture. As part of the Colorado Mycoflora Project, this study generated nrITS and nrLSU sequence data to explore the diversity of Colorado Tulostoma. Colorado Tulostoma sequence data was compared to available Tulostoma sequence data to delimit species and biogeographical ranges. Maximum-likelihood and Bayesian analyses were used to reconstruct a phylogeny of Tulostoma species. Spore morphologies were overlaid on the phylogeny and compared to species habitats and average annual precipitation to assess selective pressures of moisture on the development of spore ornamentation.
Molecular Phylogenetic Analysis to Resolve Polyphyly in an Order of Puffball Mushrooms

POSTER B14

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Abstract

The Puffball form has convergently evolved from multiple evolutionary lineages that include both poroid and gilled ancestors. The order Boletales contains puffball genera that evolved from poroid mushrooms. The objective of this study was to test for monophyly of the four Boletales genera *Pisolithus*, *Calostoma*, *Scleroderma*, and *Astraeus*. Internal Transcribed Spacer sequences that span the ITS1, 5.8s, and ITS2 from the nuclear ribosomal gene cluster were retrieved from GenBank for 96 specimens of the four genera along with outgroup sequences. These sequences were aligned in ClustalX and assembled into a maximum likelihood tree with the evolutionary model HKY+G+I using MegaX v. 10.0.5. Bootstrap analysis with 1000 replicates and a Bayesian analysis using MrBayes show that *Pisolithus*, *Calostoma*, *Scleroderma*, and *Astraeus* do not form monophyletic clades. *Pisolithus*, *Calostoma*, and *Scleroderma* formed polyphyletic clades while *Astraeus* formed a paraphyletic group. This indicates that species within these genera need a revision of their taxonomic position. The proposed phylogenetic clades and potential future studies of puffballs within the Boletales will be discussed.
Phylogenetic relationships of *Armillaria gallica* complex

**POSTER B15**

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**Abstract**

*Armillaria* is a genus of plant pathogenic and mycorrhizal fungi in the phylum Basidiomycota. Currently, *Armillaria* species from the Northern Hemisphere are well assigned in three species complexes. The *A. gallica* complex includes previously defined seven “morphological species” and ten unnamed “biological species”. However, the species delimitation of this species complex remained unclear. In this study, a phylogenetic approach is attempted to clarify the relationships of species in the *A. gallica* complex with extensive sampling from the Northern Hemisphere. The GCPSR, PTP and BP&P analyses recognized three phylogenetic species from *A. gallica* complex, i.e. *A. nabsnona* and Phylogenetic Species I (previously defined “biological species”, “Nag. E”, by Nagasawa 1991) and PS II. The PS II represents a complex species, including previously defined five “morphological species” (“*A. gallica*”, “*A. cepistipes*”, “*A. calvescens*”, “*A. altimontana*” and “*A. sinapina*”) and nine Chinese “biological species” (CBS A, CBS B, CBS C, CBS F, CBS H, CBS J, CBS L, CBS N and CBS O). The STRUCTURE analysis revealed that the PS II included three populations. One is a Chinese endemic population mainly from Qinghai-Tibet Plateau. The other two are transcontinental populations each with continentally diverged subpopulations. These results suggest that PS II is experiencing a violent genetic divergence in its allopatric speciation, and previously defined “species” are revealed to be geographic populations.
Rhodotus palmatus Does Not Occur in North America

POSTER B16

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Abstract

Rhodotus is among the most well-known macrofungal genera due to its striking morphological features of which the presence of pronounced gelatinous reticulation on the upper surface of the pileus and coral red coloration stand out. The members of this genus are decomposers of wood, primarily elm, where it is often found fruiting directly from decorticated logs. The genus was considered to be monotypic for over 80 years, with R. palmatus described from France. It was not until 2013 that a second member of the genus, R. asperior, was described from Asia. The two species differ in geographic range, spore morphology, and DNA sequences. Rhodotus is reported from eastern North America as R. palmatus. However, it has never been established these are conspecific of European R. palmatus. A study is thus performed with fifty-nine recent collections and herbarium specimens of Rhodotus from across eastern North America. For representative collections, detailed morphological and microscopic data were collected. DNA was extracted from all collections and sequenced at three loci (ITS, EF1, LSU) and compared with the two existing species. Together these data suggest that all Rhodotus species in eastern North America belong to a single, novel lineage. Taxa matching the North American Rhodotus sp. have been previously described in Lentinula, Agaricus, Clitocybe, Pleurotus, and Panus, with L. reticeps taking priority. This is another example of misapplication of European names to North American taxa.
Population genomic study of an introduced ectomycorrhizal fungus *Suillus luteus*

POSTER B17

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Abstract

*Suillus luteus* is one of the most widely-introduced ectomycorrhizal fungi in the world. During the forestation of pine around the world, *S. luteus* has been introduced to North America, South America, South Africa and Oceania from its native Eurasian distribution. We sequenced 153 *S. luteus* genomes from native and introduced populations. Phylogenetic analysis indicates that *S. luteus* populations from Australia, New Zealand, and South America each possess novel SNPs that place them into well-supported monophyletic clades. Australia and New Zealand form a single clade in the ML tree, suggesting either shared common ancestry, or recent admixture. PCA and admixture analysis support the populations in exotic areas clustered together at continental level, and that all exotic population are divergent from European source population except North American individuals. Both PCA and admixture analysis imply Australia population and New Zealand population have undergone recent admixture. These results suggest that (1) exotic populations on different continents are descended from independent colonization events (2) Australia and New Zealand likely represent two independent introduction events, while subsequent migration homogenize the genetic components (3) North American population has similar genetic components as European populations, probably reflecting recent history of introduction followed by limited population expansion and reproduction.
Presence of the invasive “death cap” fungus (*Amanita phalloides*) associated with European hornbeam trees in Kelowna, British Columbia

**POSTER B18**

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**Abstract**

The world’s deadliest poisonous mushroom, *Amanita phalloides*, known commonly as the death cap, was introduced to North America from Europe on the roots of ornamental saplings and has been expanding its range since the early 1900’s. World-wide, ingestion of this species has led to the most mushroom related fatalities on record. *A. phalloides* is an ectomycorrhizal fungus which forms a mutualistic association with the roots of a plant host. In Northwestern cities such as Vancouver and Victoria, British Columbia, death caps are most commonly found in association with European hornbeam (*Carpinus betulus*) trees. Kelowna, BC is home to many hornbeams, yet a death cap sighting has never been documented. This study aims to identify whether hornbeams in Kelowna form mycorrhizas with *A. phalloides*. The presence of mycorrhizal root tips would indicate potential to yield future sporocarps. Soil cores were taken from the base of 20 mature hornbeams around Kelowna. Root tips resembling the genus *Amanita* were isolated from these soil samples. DNA was extracted and the ITS1 region was sequenced from the root tips in order to determine the presence or absence of *A. phalloides*. The results from this study will expand the current understanding of the distribution of *A. phalloides* in British Columbia and provide the City of Kelowna with the foresight to develop a strategy to mitigate possible future poisonings.
The Subterranean Internet of Fungi: Copper Integrated Melaninized Mycelium as a Conductive Biowire

POSTER B19

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Abstract

For more than 40 years, melanin has been studied for its validity as perhaps the only conductive readily available bio-macromolecule. Though results have been mixed with several caveats, distinctive improvements have been made in increasing the electrical and photo-conductive properties of melanin. Melanin could be a promising bridge between electronics and biology and here we consider the application of melanized fungi as a method for mimicking the natural “internet” of mycelial networks present in soil ecosystems, prompting them instead to propagate weak electrical signals. These melanized networks could eventually serve as a new form of sensor for subterranean activity. Using Curvularia lunata as our base organism we assessed the conductive, resistive, and spectral properties (using FTIR) of extracted melanin in order to better understand the efficacy of this fast growing species to serve as the model framework for eventual simulated networks. We also leveraged the known capabilities of melanin to chelate metals to introduce and bind copper ions to the cell walls with the intent of improving conductivity and melanin production. The goal of this project is to eventually construct a simulated mycelial circuit and attempt to pass a weak electrical current through it and from there further study the dynamics of signal propagation through these circuits.
Effects of phosphorus fertilization and a companion plant on formation of arbuscular mycorrhizal propagules and colonization of the shrub *Artemisia tridentata*

**POSTER B20**

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**Abstract**

Nursery inoculation of shrub and tree seedlings with arbuscular mycorrhizae (AMF) can improve seedling establishment after field transplanting. The success of this practice partly depends on the extent of root colonization and the abundance of AMF propagules in the transplanted seedlings. A full-factorial combination experiment was conducted to investigate the effect of two phosphorus (P) fertilization levels, 5 and 250 µM, and the absence/presence of a companion species, the grass *Poa secunda*, on AMF colonization of *Artemisia tridentata*, the formation of vesicles and spores, and the AMF taxa present in the roots. *A. tridentata* seedlings were grown from seeds in a potting mixture containing native AMF. After eight months, the seedlings were assigned to one of the four treatments and grown for an additional five months. Total and vesicular AMF colonization of *A. tridentata* seedlings was higher in co-cultivated seedlings under low P than in the other treatments. Low P fertilization also increased AMF and vesicular colonization in *P. secunda* roots. Neither P fertilization nor cocultivation had an effect on spore density in the potting mixture. In addition, cocultivation did not affect the AMF taxa present in the roots, which were dominated by amplicon sequence variants within the *Funneliformis* and *Glomus* genera. In taxa within these genera, colonized root fragments containing vesicles are often the main propagules. Particularly in this situation, the increase in vesicle density caused by the companion plant and low P is likely to enhance AMF colonization of *A. tridentata* roots after field transplanting.
Bioremediation of oil pollutants by fungi associated with coastal mangroves in Puerto Rico

POSTER B21

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Abstract

Mangroves play an important ecological role in the coastal environment. They stabilize coastlines, reducing erosion from storm surges, waves, tides and currents. Pollution is high due to exposure to petroleum hydrocarbons (PHCs) from motorboats such as waste gasoline, diesel and motor oil leakage. These compounds have stable ring structures difficult to degrade, hence harmful to the environment and even carcinogenic. The compounds found in the PHCs also accumulate in sediments of mangroves and because of their low solubility and hydrophobic nature it is difficult to eliminate them. Nonetheless, lignolytic fungi have been found to produce extracellular enzymes capable of degrading these organic compounds. Therefore, the primary objective for this study is to isolate and characterize autochthonous fungi that can degrade PHCs. Twenty seven fungi specimens from mangrove leaves and soil samples were isolated in Potato Dextrose Agar (PDA). These were later inoculated in Congo Red Agar (MgSO₄: 0.5g, NaNO₃: [10mg/ml], H₂KPO₄: 0.5g, HK₂PO₄: 0.6g and Congo Red: [0.04mg/ml]) to determine their ability to degrade azoles. Only thirteen isolates showed growth in the media indicating possible PHC degraders. Molecular characterization was performed for six selected specimens corresponding to Talaromyces ruber, Trichoderma sp., Purpureocillium lilacinum, Aspergillus sp., Emericella sp. and Pichia guilliermondii. These fungi were inoculated in a motor oil waste liquid media (NaNO₃, aged sea water and used motor oil) to determine their capacity to degrade PHCs. Biomass production was evaluated by dry weight after 21 days of growth. Preliminary results indicate T. ruber is the fastest strain in our samples so far.
Simple and efficient mutagenesis programme to improve the antagonistic potential of *Trichoderma* biocontrol agents

**POSTER B22**

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**Abstract**

The development of new effective biocontrol agents is largely based on the antagonistic capacity of candidate agents against targeted pathogens *in vitro*. Different mechanisms contribute to such capacity, including the activity of cell wall-degrading enzymes, secretion of antimicrobial secondary metabolites, growth vigour and resistance to exogenous and endogenous toxins. In this study, a series of laboratory experiments were designed to improve the antagonistic activities of *Trichoderma* spp. against two plant fungal pathogens, *Sclerotium rolfsii* and *Rhizoctonia solani*. A simple but efficient mutagenesis programme was carried out using ultraviolet light to induce modifications in the genetic structure of two *Trichoderma* biocontrol agents, *T. virens* and *T. asperellum*. The obtained mutants were subjected to **a)** initial screening for non-volatile antifungal metabolites using cellophane membrane-based method, and **b)** selected mutants were further subjected to a series of antagonistic tests. Results revealed that the antagonistic potential of selected mutants was significantly improved against the two plant pathogens. Genetic stability test indicated that the superior UV-derived mutant Tv3, maintained its elevated performance after 12 rounds of sub-culture. Gene expression analysis for five antagonism-associated genes were examined using real-Time PCR. Results revealed that the gene expression of two genes, chitinase 33, a cell wall degrading enzyme and, polyketide synthase, responsible for polyketide biosynthesis, a class of secondary metabolites with antimicrobial roles, were significantly upregulated in one of the mutated *T. virens* strains. Results of our *in vitro* antagonistic studies along with our molecular analysis indicate that the UV mutagenesis is an effective strategy to improve *Trichoderma* antagonistic potential.
Using *Moesziomyces aphidis* and arbuscular mycorrhizal fungi to combat the *Neoerysiphe galeopsidis* (powdery mildew) on an endangered Hawaiian endemic plant

**POSTER B23**

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**Abstract**

We measured the percent infection of *Neoerysiphe galeopsidis* (powdery mildew) on the leaves of *Phyllostegia kaalaensis*, a critically endangered plant endemic to Hawaii that was treated with the endophytic mycoparasitic yeast, *Moesziomyces aphidis* (END), arbuscular mycorrhizal fungi (AMF), or a combination of both AMF and END (ANE), or none (Control). We treated the plants before infecting them with the powdery mildew and grew them in a greenhouse for 11 weeks and then measured disease severity after an additional 11 weeks of exposure to the pathogen. At the end of the experimental period the addition of *M. aphidis* significantly decreased the degree of infection in *P. kaalaensis* in both the END and ANE treatments. The AMF treatment did not show any significant difference between the control group or the END and ANE treatments, but decreased the percent of infection by 2.9% on average. This work will be used to inform conservation agencies on the best practices to increase the likelihood of survival of *P. kaalaensis* and other species affected by *N. galeopsidis* during propagation and restoration into the wild.
Mycobiome diversity in field and greenhouse potato cyst nematode populations

POSTER B24

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Abstract

Plant-parasitic nematodes are one of the most important pathogens impacting agricultural crops. Potato is a vital crop for rural livelihoods and important for food security; however, the potato cyst nematode (PCN) remains a major constraint to its production globally. *Globodera rostochiensis* and *G. pallida*, are internationally recognized and among the most damaging quarantine pests to potato, causing up to 80% yield loss. Most nematode populations are thought to be regulated by their natural enemy community. Following the restriction of synthetic nematicides, there is an urgent need for alternative methods of controlling PCN, but little data exist on how fungal species may play a role in natural control. This project aims to: 1) isolate and characterize the diversity of fungal species colonizing PCN cysts, and 2) compare the mycofloras in cysts between the different regions and identify fungi for potential use as a biological control agent. *Globodera rostochiensis, G. pallida,* and *G. ellingtonae* populations from different regions were collected and screened for fungi. These included field and greenhouse-grown populations. Surface sterilized cysts were crushed and plated in four media (potato dextrose agar, malt yeast extract, yeast malt agar, and yeast extract). Fungal growth was isolated in axenic culture. Genomic DNA was extracted from isolated fungi and amplified at the internal transcribed spacer (ITS) region and analyzed by BLASTn. Three species have been repeatedly isolated from *G. ellingtonae: Debaromyces* sp., *Aureobasidium* sp., and *Aspergillus* sp. Isolated fungi will be subjected to bioassays to assess their effectiveness as biological control agents against PCN.
Interkingdom interactions in the soybean root microbiome with different soybean seed treatments

POSTER B25

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Abstract

Soybean seeds and seedlings are vulnerable to many soil-borne pests and pathogens, and protection of emerging soybeans is essential. However, not much is known about the ecological significance of chemical seed treatments on microbial communities. The objective of this research was to investigate interactions between oomycetes, fungi, and bacteria within soybean roots and to understand if soybean seed treatments impacted these interactions through direct and indirect means. Roots were collected over two years from two locations in Michigan from treated soybean. DNA was extracted from soybean root tissue and amplicon libraries were constructed for bacteria, fungi, and oomycetes then sequenced using Illumina MiSeq. We used amplicon sequencing to investigate the ecological dynamics of bacterial, oomycete, and fungal communities in soybean roots. Co-occurrence networks were constructed and investigations into the interactions among soybean root microbes revealed that the majority of interkingdom interactions were positive. Negative interkingdom interactions could reveal potential biocontrol candidates. The investigation into the effect of seed treatment chemistry onto microbial network structure in soybean roots is underway and will reveal how seed treatment chemistry may alter network structure for improved plant health.
Hitching a Ride: Fungal Diversity Associated with Bird Populations in Utah

POSTER B26

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Abstract

Birds can transport fungal propagules externally and internally. Internal transport of fungi has been documented for yeasts, slime molds, and mycorrhizal fungi, and has been implicated in shaping fungal biogeographical patterns through dispersal to suitable habitats. However, evidence of transport by external adhesion remains scant, and consists primarily of observations of keratinophilic fungi carried on bird feathers. While birds have been shown to harbor viable fungal propagules on their feathers and are likely involved in fungal dispersal, it is unknown whether the diversity of externally transported fungi is greater within or between bird species, or if it differs between bird species. We will conduct a metabarcoding survey of the fungal internal transcribed spacer (ITS) and large subunit (LSU) regions to characterize the propagules on feathers from birds in two locations in Utah, USA. Using these data, we will present results on if diversity is greater within or between bird species and if diversity differs between bird species. Additionally, will present results on influence of bird diet, migratory patterns, sex, morphology and nesting behavior on fungal diversity. Illuminating the influence of bird species and behavior on the diversity of fungi carried on feathers is an important step in understanding how birds impact fungal biogeographical patterns.
Population genomic analyses reveal panmixia, human-mediated transport and an undescribed low-virulence sub-population of *S. musiva* across poplar plantations in North America

POSTER B27

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Abstract

Domestication of plant species has facilitated the life of human populations. While the process of domestication of plant species facilitates the procurement of marketable goods, it may also disrupt natural ecosystems leading to changes the diversity landscape of a region, such as facilitating the adaptation, migration, and other evolutionary dynamics of fungal plant diseases. A good system for studying the consequences of plant domestication as a shaping force in the evolutionary dynamics of an emergent plant disease is the interaction between Poplar trees and *Sphaeroulina musiva*, an ascomycete plant pathogen acting as causal agent of Poplar leaf spot and stem canker. Large poplar plantations are located in the American and Canadian Pacific Northwest, the American Midwest, the provinces of Quebec and Ontario in Canada, and the Southeastern states of the USA. Our hypothesis predicts that *S. musiva* populations are locally adapting to these poplar plantations, resulting in local adaptation and structured populations of *S. musiva* within geographic locations where Poplar trees are intensively cultivated. We tested this hypothesis using a population genomics framework. Our results indicate that *S. musiva* forms a single, panmictic population across North America, with very little genetic variation. In addition, a set of unique isolates with significantly lower virulence was discovered within British Columbia. These results show low degrees of local adaptation of *S. musiva* within each of the geographic regions of interest and highlight the importance of controlling contaminated plant material as sources of potential inoculum to avoid long-spread migration of important plant pathogens.
Arbuscular mycorrhizae in Nova Scotia saltmarshes: Meta-amplicon barcoding and tidal mesocosm growth trials

POSTER B28

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Abstract

Saltmarshes are vulnerable ecosystems in global decline due to cumulative natural and anthropogenic threats. These highly productive ecosystems have several crucial roles for both marine and terrestrial organisms, most notably their high primary productivity. They also stabilize coastlines and protect coastal infrastructure from storm surge events. Current restoration efforts show mixed success, with approximately 50% failing in long term coastal stabilization. Our study examines belowground saltmarsh fungal communities associated with Sporobolus (formerly Spartina) plant roots at three sites in the Minas Basin, Nova Scotia over two years. ITS2 metabarcoding was used to determine whether fungal communities differed depending on sediment type and saltmarsh age, while Sanger ITS1 & ITS2 barcoding was used to verify the presence of arbuscular mycorrhizal symbionts of the dominant saltmarsh plant Sporobolus pumilus (formerly Spartina patens). Saltmarsh sediment fungal communities were shown to be dependant on the aboveground flora and sediment type. Funneliformis geosporum (Glomeromycota) formed a strong symbiosis with S. pumilus at all three sites examined, although colonization rates differed between sites. Native F. geosporum propagated in trap pot culture was used as an arbuscular mycorrhizal inoculant for sterile tissue culture reared rhizome and seeds of S. pumilus. In tidal mesocosm growth trials, F. geosporum increased S. pumilus survival, plant size and growth rate, making it a prime candidate for transplant and sediment priming prior to saltmarsh restoration. F. geosporum will be used in future restoration efforts to increase plant survival and improve saltmarsh restoration success.
Variation in tannin tolerance among root associated fungi

POSTER B29

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Abstract

Tannins are plant defense compounds found in bark, leaves and roots that can inhibit fungal growth by a variety of mechanisms. As conifer roots are colonized by a diverse array of fungi, it is likely that at least some groups are tolerant to tannins. We compared the effect of both tannic acid (hydrolysable) and spruce root tannins (condensed) on the survival and growth of a range of root associated fungi, including ectomycorrhizal, pathogenic and root endophytic species. Levels of tannin tolerance were mapped onto an 18S tree of the fungi tested to determine which phylogenetic groups contained tannin tolerant species. Surface sterilized spruce roots were also plated onto tannin-amended media to select for tolerant fungal species. Ectomycorrhizal fungi were highly sensitive to tannins, while most other fungi were somewhat more tolerant. However, species of dark septate root endophytes (DSEs) in the Dermateaceae and Vibrisseaeeae (e.g. Phialocephala spp.) were notably more tolerant than others. This pattern was similar for both condensed and hydrolysable tannins. Although the DSEs produce polyphenol oxidases (e.g. laccase), which eventually detoxifies the tannin, this does not appear to be the main mechanism of tolerance. We hypothesize that tannin tolerance facilitates the intracellular colonization of conifer roots by this group of dark septate endophytes.
Differential colonization by ecto-, arbuscular and ericoid mycorrhizal fungi in forested wetland plants

POSTER B30

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Abstract

Although the roots of most plants are colonized by mycorrhizal fungi under normal soil conditions, the influence of soil moisture on different types of mycorrhizal symbioses is poorly understood. In wet soils, colonization of woody plants by ectomycorrhizal (ECM) fungi tends to be poor, and colonization of herbaceous plants by arbuscular mycorrhizae (AM) is highly variable. However, little information is available on the influence of soil moisture on the colonization of ericaceous roots by ericoid mycorrhizal fungi (ErM). We studied the colonization patterns of these three mycorrhizal types along soil moisture gradients from upland forests to forested wetlands in Nova Scotia. Colonization was assessed microscopically in two ECM plants (*Abies balsamea* and *Pinus strobus*), two AM plants (*Cornus canadensis* and *Trientalis borealis*) and two ericaceous plants (*Kalmia angustifolia* and *Gaultheria hispidula*). For the two ErM plants, mycorrhizal community structure was also assessed along the soil moisture gradient by sequencing the fungal ITS. Our data agrees with previous reports on the influence of soil moisture on colonization patterns of ECM and AM, but indicates that ericoid mycorrhizal colonization may increase with soil moisture in forested wetlands.
Importance of phosphorus and AM fungal communities in performance of blanketflower, *Gaillardia aristata*, across the northern tier

**POSTER B31**

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**Abstract**

Arbuscular mycorrhizal fungi (AMF) provide nutrients such as phosphorus to their hosts in exchange for lipids and sugars. We sought to address how patterns of mycorrhizal abundance and formation and AMF community composition might vary with spatial variability of abiotic factors that should influence the importance of the symbiosis to the plant. We measured plant biomass, plant and soil nutrients, hyphal length in the soil and root colonization by AMF for *Gaillardia aristata*, a native prairie wildflower and species of special concern in Minnesota, at each of 12 sites from Montana to Minnesota that ranged in mean soil phosphorus availability from 2-38 ppm. We also grew *G. aristata* in the greenhouse with and without mycorrhizas and fertilized with or without phosphorus to determine mycorrhizal responsiveness. We identified AMF species present in the roots in the field and the greenhouse using next-generation DNA sequencing. Plants from soils with higher phosphorus availability were larger and had greater phosphorus content in their aboveground tissues. Greater plant phosphorus was associated with greater hyphal length in the soil. In the greenhouse, differences in biomass between phosphorus levels were evident only in non-inoculated plants, suggesting mycorrhiza formation alleviated phosphorus limitation. The molecular data show that at the regional scale, AMF community composition reflects geography and soil phosphorus. These results together suggest that phosphorus may limit growth in this plant species, that AMF are important for its performance in both the field and greenhouse, and that AMF community composition is influenced by different phosphorus environments.
Deciphering the role of context dependency in the community assembly of root-associated fungi

POSTER B32

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Abstract

Community assembly theory posits that dispersal, abiotic filters and biotic interactions shape local communities, but the relative importance of each of these filters often varies among communities. One explanation is that assembly filters may commonly interact. For example, results interpreted as abiotic filtering could be conflating abiotic filters that prevent species from establishing with abiotic conditions that alter species interactions. Here we asked: Do abiotic conditions modulate species interactions and shift the composition of root-associated fungal communities? We reciprocally transplanted grass seeds and fungal spores between high and low elevations in the Colorado Rocky Mountains to capitalize on the strong abiotic gradients driven by altitude. Seeds of *Festuca thurberi* and *Festuca saximontana* were placed in sterile in-ground cylinders at low or high elevation sites then inoculated with fungal spores from low or high elevations. Controls did not receive spores. Each fungal treatment (low, high, control) and elevation location (low, high) combination was replicated 9 times and repeated across 3 unique elevation gradients. We assessed how elevation affected the development of fungal community in the roots by sequencing the ITS2 region, and we determined how elevation altered the biotic interactions among fungi using pairwise Spearman rank correlations among OTUs within a site. We tested for the relative importance of abiotic filtering in the community assembly of root-associated fungi by creating structural equation models to partition the direct effects of elevation on community structure from the indirect effects via host plant identity or fungal interactions, assessed by the changes in the correlation matrix.
Effects of *Darksidea* on *Bouteloua gracilis* Germination and Growth

**POSTER B33**

**John Nichols, María-José Romero-Jiménez, Andrea Porrras-Alfaro**

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**Abstract**

Climate change and the rapid growth of human population represent major challenges for humanity. The semi-arid regions make up a third of terrestrial ecosystems and in these areas agricultural production is highly limited by environmental conditions. However, a better understanding of plant-fungal interactions in semiarid plants could improve productivity and conservation. *Darksidea* is a grass endophyte with a broad distribution in south central United States. The objective of this research was to evaluate the effects of *Darksidea* isolates on the germination and health of blue grama (*B. gracilis*). Representative isolates from eight operational taxonomic units were evaluated in plant-fungal bioassays. Non-sterile seeds were planted in sterile sand. Seeds were inoculated with fungal solutions, incubated for 20 days, and harvested. Plant and root length and number of leaves and roots were recorded. *Darksidea* root colonization was observed through phase contrast microscopy. The *Darksidea* isolates tested were recovered from blue grama, black grama (*B. eriopoda*), buffalo grass (*B. dactyloides*), and big bluestem (*Andropogon gerardii*) from Texas, New Mexico, Kansas and Wyoming. Preliminary data show a range of responses from pathogenic to mutualistic depending on the conditions. Some isolates improved root length while others decreased plant length. These results suggest a broad range of complex symbiotic responses between different *Darksidea* isolates and blue grama.
Identification of dark septate endophytes in *Artemisia tridentata* roots and their interactions with arbuscular mycorrhizae

POSTER B35

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Abstract

Roots of the shrub *Artemisia tridentata* (big sagebrush) form symbioses with dark septate endophytes (DSE) and arbuscular mycorrhizal fungi (AMF). Presently, little is known about the effect of DSE on *A. tridentata*. To gain knowledge in this area, we have isolated DSE from *A. tridentata* roots. Four distinct isolates have been identified based on sequences from the ITS and LSU regions of ribosomal RNA genes; three of the isolates are in different genera within the Pleosporales (*Darksidea*, *Montagnula*, and *Helminthosporium*) and a fourth, *Cadophora* is in the Helotiales. A re-synthesis experiment involving inoculation of *A. tridentata* seedlings *in vitro* with *Darksidea* sp. ascertained that this fungus is a root endophyte of the seedlings and does not have pathogenic effects. In addition, an experiment was conducted in soil to assess the effect of inoculation with *Darksidea* sp. on colonization by the AMF fungus *Rhizophagus irregularis*. Seedlings only inoculated with *R. irregularis* had levels of AMF colonization similar to those co-inoculated with *R. irregularis* and *Darksidea* sp. Also, seedlings only inoculated with *Darksidea* sp. had levels of DSE colonization similar to those co-inoculated with *R. irregularis* and *Darksidea* sp. These results suggest that in the species tested, the presence of DSE does not affect colonization by AMF and vice versa. Currently, we are completing the re-synthesis experiments with the other DSE isolates as well as analyzing their effect on AMF colonization.
Differential plant growth effects by soil fungi in the Mortierellaceae

POSTER B36

Natalie Vande Pol, Patrick Edger, Gregory Bonito

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Abstract

Mortierellaceae fungi are frequently isolated and detected in living plant roots, yet the ecology of these organisms is poorly understood. Molecular studies are usually unable to identify Mortierellaceae at higher taxonomic resolution, so ecological findings are often generalized across the lineage. Some Mortierella species have been found to promote aerial plant growth and flower production. To determine whether these impacts are conserved traits across Mortierellaceae we measured above-ground dry biomass and seed biomass in Arabidopsis thaliana plants grown with a panel of Mortierellaceae species from 7 ITS-based clades. We hypothesized that species within clades would have relatively consistent growth effects, but anticipated variation in growth effect between clades.

We found that uninoculated grain (millet and pearled barley) controls significantly reduced aerial plant growth as compared to a no-grain control. Most species of Mortierellaceae tested partially protected Arabidopsis and Brachypodium from the negative effects of the inoculum. The degree of plant growth promotion over controls was variable both within and between clades, indicating that growth promotion under these conditions may not correlate with phylogenetic relatedness. Our studies also indicate that inoculating soils using grain can have unintended consequences on plant growth studies, possibly due to nutrient sink or allelopathic effects. Thus, we are developing an agar-based assay to measure aerial Arabidopsis growth under otherwise sterile conditions and without the issue of grain inoculum. Roots and mycelium will be processed for transcriptome analysis to further study Mortierellaceae-Arabidopsis interactions.
Are Mycoheterotrophs Actually Parasites? Investigating the Mycorrhizal Ecology of Four California Native Plant Species

POSTER B37

Christopher Bivins, Alija Mujic
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Abstract

Mycoheterotrophic (MH) plants are plants that evolved to lose the ability to photosynthesize. They obtain all of their carbon from nearby photosynthetic host plants via mycorrhizal fungi. Because they do not contribute any carbon to the mycorrhizal network, MH plants have been classified as parasites throughout the literature. However, this carbon-focused perspective ignores MH plants’ role regarding other important elements. Additionally, no studies have been conducted that show a net decrease in fitness on either hosts as a consequence of this tripartite symbiosis. MH plants associated with ectomycorrhizal fungi display an extreme level of fungal host specificity. One potential outcome from this extreme host specificity is a competitive advantage for the ectomycorrhizal host plant and fungus due to proliferation of the hosts’ ectomycorrhizal root tips near the MH symbiont; an effect demonstrated in at least one MH species. Taken in context, the evidence used to support the designation of MH plants as parasites is inadequate. The goal of this project is to investigate these plants’ true ecological nature. We have chosen four species of MH plants to investigate: Allotropa virgata, Corallorhiza maculata, Pterospora andromedea, and Sarcodes sanguinea. We use metagenomic barcoding to determine the extent of root colonization by these species’ fungal hosts. Phosphatase assays of ectomycorrhizal roots and soil near the MH inflorescences are used to determine the effect of MH symbioses upon the phosphorus economy of their hosts. Taken together these result will allow us to support more concrete theories surrounding the ecological role of MH plants.
Effects of High Severity Wildfires on Ponderosa Pine Ectomycorrhizal Fungal Communities

POSTER B38

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Abstract

Ectomycorrhizal (EcM) fungi have the ability to mediate ecosystem responses to post-fire environmental changes, yet we have limited understanding of how high-severity wildfires influence the EcM community of ecosystems adapted to low-severity fires. In order to determine the changes to the community composition, succession of EcM fungi, and their association to soil biochemical aspects, we analyzed soil via Next-Generation sequencing using ITS1F/ITS2 across a chronosequence of four, high-severity (HS) burned, ponderosa pine (\textit{Pinus ponderosa}) stands in eastern Washington, that burned from 2006-2015. High-severity fires altered the EcM community of \textit{P. ponderosa}, resulting in a system dominated by Ascomycota, including taxa in the genera \textit{Wilcoxina}, \textit{Pustularia} and \textit{Cenococcum}. Additionally, differential analysis showed that one genera of Basidiomycetes, \textit{Lyophyllum}, responds positively to fire. Community composition did not converge to that of unburned forest after an eleven-year period, with only \textit{Wilcoxina rehmi}i dominating both communities. Soil nutrient composition, total phosphorus, and total nitrogen:total carbon ratios, as well as various abiotic factors including depth of organic matter, distance to live tree, elevation and slope strongly predicted changes to the EcM community composition. These results suggest that high-severity wildfires significantly alter the EcM community of fire-adapted ecosystems, possibly selecting for fire-adapted species such as \textit{W. rehmi}, but with time-since-fire, the alteration to the soil environment and host presence or absence can significantly influence the overall community; thus selecting for species that are poor competitors, but better adapted to survive in nutrient-limited environments.
Sixty years of prescribed fire has no effect on ectomycorrhizal communities in longleaf pine forests

POSTER B39

Ayanna Castro-Ross, Sam Fox, Ari Jumpponen, Mac Callaham
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Abstract

Wildfire severities and frequencies have increased in recent years. A tool to control fuel loads, which increase the susceptibility of forest stands to wildfires, is to utilize controlled prescribed fires. However, the extent to which soil-inhabiting microbial communities respond to such fire management is poorly known. Host-associated symbiotic fungi may be particularly sensitive to fire disturbance because they are not only impacted by the direct effects of the fires such as the heat pulses and subsequent rollercoaster of inorganic nutrient dynamics, but also by the indirect effects through shifts in host metabolism. We aimed to quantify the effect of fire exclusion on the ectomycorrhizal fungal communities associated with roots of longleaf pine (Pinus palustris) in an experimental prescribed burn program at the US Forest Service’s Olustee Experimental Forest, wherein 1-yr, 2-yr and 4-yr fire frequencies have been maintained for nearly six decades and can be contrasted against complete fire exclusion in longleaf pine stands. We sampled ectomycorrhizal roots from the A horizon in the coastal sandy soils in 2018, stored them in 90% EtOH and dissected the fungal communities using an expedient experimental protocol that permits direct PCR-amplification of DNAs without separate nucleic acid extraction steps. Analyses of ectomycorrhizal roots provided no evidence of adverse effects of prescribed burns on ectomycorrhizal communities. Our data suggest that ectomycorrhizal communities are adapted to repeated low-intensity fires in this coastal coniferous ecosystem.
The biology and distribution of morels in Southern Chile: the balance between forest sustainability while supporting a morel-gathering economy.

POSTER B40

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Abstract

The harvesting of morels is a vital economic activity for local communities in Chile because they are a significant commercial export for this country. Although many species of morels produce ascomata in the absence of fire, abundant ascomata production occurs among phoenicoid Morchella species when triggered by fire. The intentional burning of Nothofagus forests in Southern Chile, as a means to increase morel production, has become a problem and has negatively impacted ecosystems. To better understand which Morchella species are being commercially harvested in Southern Chile, molecular markers were used to identify collections of morels being harvested and/or sold commercially and determine their phylogenetic relationships with other Morchella species. Morels were sampled from collections in the FFCL Fungarium and batches purchased from commercial harvesters and bulk gatherers in 2015 and 2016. DNA sequence from the LSU, ITS, RPB1, RPB2 and EF1a were obtained. Phylogenetic analyses of the ITS and RPB1 sequences determined that the 13 specimens collected from southern Chile belong to the Elata Clade and were either in the M. frustrata/Mel-2 lineage or the Mel-37 lineage which is recognized by Pildain et al., 2014, as a unique lineage; none of the collections were part of the “fire adapted lineage” of Morchella/Mel-6 to Mel-10. These results support the success of harvesting morels in the absence of destructive burning practices. Such information will be useful in outreach programs to local communities to help promote and develop sustainable practices for commercial morel harvesting and discourage destructive burning practices.
Genomic insights into reproductive strategies and successional patterns of fire-associated *Morchella*

POSTER B41

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Abstract

Burn morels are found in montane, conifer forests in the northwestern United States in the years immediately following a wildfire. They are one of the earliest emerging organisms in fire-disturbed habitats, often occurring in very large numbers. While these mushrooms have economic and ecological importance, little is known about many aspects of their basic biology, including how many years they reproduce sexually after fires and the relative importance of sexual vs. asexual reproduction between fire events. To address their fruiting duration, we collected second-year post fire specimens from sites where wildfires occurred in 2017 and burn morel species were collected in 2018. New specimens were identified using DNA sequencing to determine whether burn morels continue to reproduce or whether succession of non-fire-associated morel species predominate in the second-year post-fire. To address their reproductive styles, we surveyed both first- and second-year post-fire sites and are using genomic data to reveal the spatial extent of genetic individuals in order to determine population genetic structure within and between sites. Results from this research will aid the management of wildfire-prone lands and inform collection practices and tools to aid in predicting burn morel emergence by creating a better understanding of these commercially and ecologically important mushroom species.
Analysis of the Effect of Wildfire on Fungal and Bacterial Soil Communities Using Pre- and Post- Fire Samples

POSTER B42

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Abstract

Wildfires and the more recent “Mega-Fires” create major disturbances with lasting impacts on soil microbial communities. Climate change is increasing the frequency of these radical wildfire events. Currently, most research on post-fire microbial communities is limited to the Pinaceae. The Soberanes Fire of 2016 presented a unique opportunity to study the effect of wildfire on soil microbial communities in a non-pine forest. The fire burned a large area in Big Sur, CA including several established plots for studying soil microbial communities in redwood-tanoak forests.

In this study we examined the pre-fire and post-fire microbial community in 3 plots (2 burned, 1 unburned) to assess the effect of a Mega-Fire on soil microbial communities. All plots were located in California Redwood (Sequoia sempervirens) and Tanoak (Notolothocarpus densiflorus) forests of Big Sur, CA. Microbial communities were analyzed using Illumina MiSeq sequencing of ITS1 and 16S rRNA genes for fungi and bacteria, respectively.

We hypothesized both microbial diversity and abundance would be significantly diminished post-fire in the burned sites while the unburned site should not differ significantly from the pre-fire data. We found that while both bacterial and fungal communities were reduced in alpha and beta-diversity after the fire, certain groups of taxa appeared to increase in frequency after the fire. Most excitingly, similar to a Mega-Fire in a California Pine forest, genera of truffle forming fungi increased in frequency after the fire. Thus, generalizable traits of fire adapted fungi are beginning to emerge.
Where are they hiding? Testing the body snatcher hypothesis in pyrophilous fungi

POSTER B43

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Abstract

Pyrophilous fungi are known to produce sporocarps after a fire but little is known about their ecology prior to or after a fire event. Recently, Matheny et al. (2018) proposed that some post-fire fungi form endophytic and/or endolichenic relationships with plants and lichens based on ITS sequence similarity between post-fire fungal sporocarps and endophytic and/or endolichenic fungi, observations also noted by others. Matheny and colleagues described this as the ‘body snatcher’ hypothesis. In order to test the body snatcher hypothesis, bryophyte, lichen, club moss, and soil samples were collected from unburned and mixed-intensity burn areas one year and two years after a 2016 wildfire in the Great Smoky Mountains National Park and from unburned areas in four states outside the park, and examined for the presence of pyrophilous fungi occurring as endophytes using culture-dependent and culture-independent techniques. Culture-dependent methods isolated Pholiota highlandensis, a known pyrophilous fungus, from several bryophyte samples. Culture-independent methods identified 22 pyrophilous taxa from bryophyte, club moss, lichen, and soil samples across a range of geographical localities. The ‘body snatcher’ hypothesis is supported since many bryophyte, lichen, and club moss samples contained pyrophilous taxa suggesting that these fungi occur as endophytes and/or endolichenic fungi until a fire event triggers them to produce sporocarps
A new nematode trapping *Orbilia* from Puerto Rico

**POSTER B44**

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**Abstract**

Little is known about the diversity of Orbiliomycetes from Puerto Rico. Cantrell & Lodge (2008) compiled a list of the fungi from Puerto Rico, and only mentioned four species of *Orbilia*: *O. andina*, *O. chysocoma*, *O. delicata* and *O. cf. gaillardii*. During IMC11 in Puerto Rico, 2018, several collections of Orbiliomycetes were found in Juan Enrique Monagas Park during the Ascomycete workshop field trip. Some of these were sent to the Cornell and Farlow Herbaria. One collection caught the attention of Luis Quijada due to its interesting morphological features. This species is not related to any of the species reported by Cantrell & Lodge (2008). The morphology of the asci and ascospores of the sexual morph clearly indicates a relationship with *Orbilia auricolor* and related species (section *Arthrobotrys*). The morphology of the strongly mammiform paraphyses and the excipulum with large cortical cells with knob-like glassy caps had never before seen in this section. Our cultures produced an *Arthrobotrys*-like anamorph most similar to the anamorph of *O. blumenaviensis* (= *A. vermicola*), but the conidia are distinctly smaller and never more than 1-septate. Molecular data supports the placement of this *Orbilia* in series *Arthrobotrys*. Species in this series produce adhesive networks as trapping organs in the presence of nematodes, and this behavior was confirmed in cultures of this *Orbilia*. Our phylogenetic analysis shows this species as very distinct from *O. blumenaviensis* and supports it being new to science.
Investigating the degradation of thermally-modified plant biomass by fire-adapted fungi

POSTER B45

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Abstract

Efforts to convert plant biomass into fuels and other bio-based products are increasingly focusing on thermal methods. These methods offer several key advantages over enzymatic deconstruction routes, including being ‘agnostic’ to the type of biomass being treated. Heat-modified residues, however, still require enzymatic processing, and current enzyme ‘cocktails’ are not optimized to these tasks. Our goal is to identify novel biomanufacturing enzymes from a logical organism source, fire-adapted fungi, by first investigating the ability of these fungi to degrade thermally-modified plant biomass. Fire-adapted fungi are commonly observed growing on charred plant biomass after wildfires and likely possess a unique suite of enzymes used for degrading thermally-modified plant residues. One well-studied example is Neurospora crassa. This Ascomycete fungus has been studied thoroughly out of the context of its natural niche on fire-killed plant biomass, but has nonetheless become a model organism with well-established genetic tools. These tools can, however, be utilized to study N. crassa within its natural niche, which may help elucidate specific enzymes and mechanisms involved in the degradation of thermally-modified plant biomass. There are many other fungal genera (e.g. Antrodia, Dichomitus, Gloeophyllum) associated with fire as well, many of which have annotated genomes in the Joint Genome Institute portal, and elsewhere, which may prove useful in investigating gene functions. Tapping into these fire-adapted fungal systems may reveal genes with more relevance to thermal deconstruction processes and with more potential for tailoring to biomanufacturing processes ‘downstream.’
Are Sweden’s forest conservation values linked to soil carbon stock size and belowground fungal diversity?

POSTER B46

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Abstract

Forest management has shaped Sweden’s landscape for decades, modifying soil processes and composition. The allocation of forest stands for harvesting, biodiversity conservation or carbon sequestration depends on indirect assessments of stand age and structure, so the diversity of the fungal community and size of soil carbon stocks affected by this decision remains unknown. Soil fungal community composition has important ramifications for the carbon sequestration since these organisms mediate organic matter processing in boreal forest soils. Scaling up process rates and organic matter estimates linked with microbial community data is challenging because the sampling strategy for representing stands remains uncertain. Therefore, we planned to uncover proper sampling efforts by physically or computationally pooled 20, 40, 60 or 80 cores taken systematically across 2-hectare stands in four production forests and four woodland key habitats. Total fungal communities have been quantified and identified using metabarcoding of the species level fungal DNA barcode ITS2 and PacBio sequencing. This result will inform our further sampling of 80 stands across the full range of boreal forest in Sweden, representing a gradient in conservational values based on various other indirect and direct biodiversity assessment methods. We hypothesize that stands with a higher conservation value support higher richness and evenness of species. Furthermore, we expect the soil carbon stock to be related to the soil fungal community composition rather than the richness. In the boreal forest, this type of data will inform whether currently used forest value assessments are linked to carbon sequestration and soil fungal diversity.
How fungal pathogens shape prairie plant diversity

POSTER B48

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Abstract

Given rapidly changing climate conditions and loss of preserved prairie ecosystems, it is crucial to understand the drivers of existing biodiversity maintenance so that we can protect prairie plant species from risk of extinction. The vast majority of Midwestern prairie grassland has been converted into crop production land, causing decreases in native plant diversity and creating more barriers for the survival of many plant species. Accumulative evidence suggests that plant pathogens drive plant community diversity. This increased impact of pathogens has been observed in plant communities with low plant diversity, i.e. monocultures. In order to better understand the relationships between plant diversity and pathogen abundance, plots at the KU Field Station have been manipulated in various dimensions, including plant diversity. These plant diversity plots were seeded with the three plant families with varying traits, Poaceae, Fabaceae, and Asteraceae. These plants were then arranged in monoculture, or contained 2, 3, and up to 6 different plant species in one 1x1 m area. Soil samples were collected from each of the plant diversity treatments, and following DNA extraction, these samples were sequenced for fungal and Oomycete OTUs. Using bioinformatics programing, we identified correlations between plant pathogen abundance and diversity with plant community composition and diversity to test our hypotheses. We expect fungal pathogen relative abundance to decrease as plant diversity increases, with a positive correlation between fungal plant pathogen diversity and plant diversity.
On the Origin of Feces: Investigating Truffle diversity and distribution with metagenomic amplicon sequencing of scat material.

POSTER B49

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Abstract

The Kingdom Fungi is an extremely diverse group of life which are ubiquitous across the globe, with ~120,000 species currently known. Often, the extent of diversity and distribution of fungal communities is difficult or near impossible to assess. This is due to the fact that many Fungi are cryptic and persist predominantly within substrates. This is particularly true for hypogeous fruiting bodies, such as truffles, which are extremely difficult to survey in any kind systematic manner. However, fungi with hypogeous fruiting body morphology have evolved traits making them highly attractive to animals, such as small rodents, which ingest and disperse fungal spores through defecation. Here, samples of scat from over 100 rodents in the western United States were assessed for fungal diversity using a metabarcoding approach. The ITS2 and 5′-prime region of the LSU were amplified using three sets of custom-indexed primers selected to minimize taxonomic bias. Amplicons were normalized and pooled before Illumina adapters were ligated in a single library, which was sequenced on one lane of 2 x 150 PE HiSeq. Our data show that the majority of fungal sequences from scat samples are assignable to Agaricomycetidae, with most belonging to several species of the hypogeous truffle genus Rhizopogon. From our data, rodent taxonomy did not predict fungal species, but instead, fungal species were correlated with habitat. Combined with geographic coordinates from trapped rodents, this approach makes it possible to generate a more complete understanding of local hypogeous fungal diversity and distribution.
Using phylogenetic specificity symmetry to compare bipartite networks of lichens, endophytes and mycorrhizae

POSTER B50

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Abstract

In network analyses, specificity and the symmetry of specialization have been proposed to be drivers of species abundance and geographic range, whole-network stability, modularity, and coevolutionary dynamics. In several systems, symbiont switches and host range have been shown to be phylogenetically constrained. However, network ecology has yet to incorporate phylogenetic information when measuring specificity and specialization symmetry. Several diversity indices now include phylogenetic information and have been used extensively in studies of host-parasite interactions to assess host-specificity. However, these tools only map specificity onto the phylogenies of one partner. We use existing metrics of phylogenetic alpha diversity to estimate species level and whole-network specificity and specificity symmetry in an interaction network between lichen-forming fungi and their Nostoc symbionts, as well as endolichenic fungi and ectomycorrhizal fungi and their respective hosts. We compare these results with estimates from currently available network specificity metrics.
Microbiome of the Cultivated Morel (*Morchella* spp.)

**POSTER B51**

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**Abstract**

Morels (*Morchella* spp.) are iconic edible mushrooms with a long history of use. Recent advances have led to successful cultivation of morels in outdoor habitats, where they are grown in non-sterile soils and substrates. Some microbial taxa are hypothesized to be important in triggering the formation of primorida and development of fruiting bodies, thus, there is interest in the microbial ecology of *Morchella*. We used ITS and 16S amplicon sequence data to identify and compare fungal and bacterial communities in substrates where *Morchella sextelata* is cultivated in outdoor growhouses. We found that Pedobacter, Pseudomonas, Stenotrophomonas, and Flavobacterium comprise the microbiome of *M. sextelata*. These bacterial taxa were also abundant in substrates beneath growing fruiting bodies. The soil microbiome beneath morels cultivated in soils was dominated by *Morchella*, Mortierella, Clonostachys, and Phialocephala. This research informs our understanding of microbial indicators and potential facilitators of *Morchella* productivity.
Do fungal endophytes facilitate colonization of bacterial endophytes in *Brachypodium distachyon*?

**POSTER B52**

Julian Liber, Gregory Bonito

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**Abstract**

Endophytic bacteria and fungi are ubiquitous within plant tissues. These microorganisms may affect their plant host via hormonal signaling and can improve the host’s stress tolerance. In nature, communities of fungi and bacteria infect plants as they grow, but the mechanism of bacterial movement into plant tissues, especially roots, is poorly understood. Enhancement of bacterial colonization could make beneficial bacterial inoculants more effective. Bacteria are known to move through soil and cheese using the water layer on hydrophilic fungal hyphae through various motilities, but it is unknown if the bacteria use these mechanisms to enter plant roots. We tested this using the bacterium *Enterobacter ludwigii*, multiple diverse fungi isolated as endophytes, and the model grass *Brachypodium distachyon*. Volatiles from the bacteria were observed to have either positive or negative effects on radial growth of target fungi, and bacteria were observed moving along hyphae on agar plates. In axenic plate culture with *B. distachyon*, the bacteria resulted in decreased shoot biomass and increased root hair length. Plants co-inoculated with fungi had reduced infection by the bacteria, contrary to the expected facilitation of bacterial colonization by fungal root colonization. We suspect that fungi and bacteria are competing for niche space within the apoplast of roots, but finer scale resolution of this relationship is still needed. In summary, we found no evidence of facilitation of root endophyte colonization by root endophytic fungi. Fluorescent microscopy and use of additional organisms will be used to further understanding of the mechanisms of rhizospheric bacterial-fungal interactions.
Curating *Colletotrichum* sequence records – an NCBI and APHIS collaboration

POSTER B53

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Abstract

Publicly available DNA reference sequences derived from a suitable taxonomic reference source are critical to the identification efforts of plant protection organizations, such as the United States Department of Agriculture, Animal and Plant Health Inspection Service, Plant Protection and Quarantine (USDA-APHIS-PPQ), and plant health professionals. Development and curation of such data for important pest taxa such as *Colletotrichum* serve to increase confidence and quality of identifications. In turn this improves knowledge of host and geographic ranges, understanding of risk, and ultimately regulatory action and policy. *Colletotrichum* species are often morphologically cryptic and among the most frequently regulated plant pathogens by APHIS. The ITS RefSeq Targeted Loci (RTL) database for Fungi at NCBI (BioProject PRJNA177353) currently contains sequence records for more than 10,000 species including 181 orders and 2,231 genera. It interacts extensively with the NCBI Taxonomy database, a separately managed resource that provides a central reference for species names and type material information. The RefSeq ITS database contains curated sequence records of more than 200 *Colletotrichum* species, serving as a public source of sequence – type strain – name associations. Within each RefSeq record, strain identifiers are linked to a public biocollection. At APHIS, these associations were verified for each of these species for up to eight loci. Conspecific strains were also gathered and verified to create a larger database containing intraspecific variation. We present examples of this database’s utility in a variety of settings and indicate improvements made to all 3 mentioned resources as a result of this collaboration.
New species of *Laboulbenia* (Laboulbeniales, Ascomycota) on two new host families, Gerridae and Thyreocoridae (Hemiptera, Insecta)

**POSTER B54**

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**Abstract**

Seven new species of the genus *Laboulbenia* (Laboulbeniales, Ascomycota) are described from two new host families, Gerridae and Thyreocoridae, within the suborder Heteroptera (Hemiptera, Insecta). Previously, only 11 of the approximate 800 described species of *Laboulbenia* were known to occur on Heteroptera. These seven new species, *Laboulbenia brachymetrae, L. cylindrostethi, L. neogerridis, L. tachy Gerridis, L. pedunculata, L. thyreocoridis, L. antherbotrus*, are described from five countries within Central and South America—Bolivia, Brazil, Panama, Peru, and Venezuela. The newly described fungi are compared with known species, and illustrations and photographs accompany the descriptions.
Phylogenetic placement of the Geoglossomycetes based on whole-genome data

POSTER B55

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Abstract

The taxonomic classification of the under-studied class, the Geoglossomycetes (Ascomycota, Pezizomycotina) has been ambiguous, resulting in many shifts in its placement. Traditionally, our understanding of the phylogenetic placement of the Geoglossomycetes was based on morphological data and observations. More recent classifications using concatenated alignments of a small number of genes have illuminated the relationships within the class. As technology and pipelines of next-generation sequencing improve, we can continue revising the taxonomy of the group through the examination of entire genomes. In this study, phylogenetic analysis of genome-scale data of several species within the class has provided further insight into the taxonomy of the Geoglossomycetes. We have constructed phylogenies using hundreds of target genes to reassess the hypothesized placement of this class within the Ascomycota. Using this data, we present an analysis of Geoglossomycetes alongside the closely related class, the Leotiomycetes, to uncover evolutionary patterns in the fruiting body morphology of these two lineages.
Black spot fungi on rosaceous hosts: *Diplocarpon* represents a unique evolutionary lineage within Leotiomycetes

**POSTER B56**

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**Abstract**

The black spot diseases of rosaceous hosts are primarily caused by the species of *Diplocarpon*, formerly known as *Marssonina*. Species of *Diplocarpon* cause severe diseases on several economically important hosts, including garden roses, apple, pear, and strawberry. However, the precise phylogenetic placement of these species is not well understood. In the present study, we used fresh collections and herbarium specimens to infer molecular phylogenetic placement and to clarify the taxonomy and nomenclature of this poorly known group of phytopathogenic fungi. The molecular phylogeny based on 28S and ITS rDNA sequences and including the type species of the genus, *Diplocarpon rosae*, revealed that the genus represents a unique evolutionary lineage within the Helotiales. Two additional species, *Diplocarpon fragariae*, causing leaf scorch disease of strawberry, and *Diplocarpon coronariae*, causing black spot of apple and pear, grouped with the type species and could be distinguished using sequence data. In addition, type specimens of other species in the genus were studied and distinguished based on morphological characters. These species of phytopathogenic fungi were found to grow poorly on artificial media thus limited amounts of molecular data and cultures were available in public databases. However, this study contributes towards a stable platform for the taxonomy of obscure genera of phytopathogenic fungi.
Phylogenetic Analyses of the Genus *Platismatia* (Parmeliaceae, Lichenized Ascomycetes) Shed New Light on Species from Northeastern North America

**POSTER B57**

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**Abstract**

Few studies on the relationships between species within the genus *Platismatia* using molecular phylogenetic analysis have been published. Only one previous study specifically focused on the molecular phylogeny of *Platismatia*. This study used few sequences and did not include all of the species in the genus. In our study, new sequences (n=44) of *Platismatia* (*P. glauca* (n=17), *P. herrei* (n=3), *P. lacunosa* (n=2), *P. norvegica* (n=3), *P. stenophylla* (n=2), *P. tuckermanii* (n=11), and *P. wheeleri* (n=6)) were generated. Representatives of *P. glauca*, *P. norvegica*, and *P. tuckermanii* from Northeastern North America were sequenced as part of this sampling. Particular interest in the resulting phylogeny related to the clade including *P. glauca*, *P. tuckermanii*, and *P. wheeleri*. *Platismatia glauca* is a cosmopolitan species which was recovered into two separate strongly supported sister clades. Each clade contained species from both Europe and the Americas. We confirm that *Platismatia* contains several asexual and sexual species pairs, for example *P. glauca* (asexual) and *P. tuckermanii* (sexual) as well as *P. herrei* (asexual) and *P. stenophylla* (sexual).
Survey of Marine Yeasts associated with Mangroves in Puerto Rico

POSTER B58

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Abstract

Marine yeasts are widely distributed in marine environments depending on organic materials and other factors. Marine yeasts can be isolated from sea-water, sediments, plants of marine habitats and digestive tracks of marine animals. They have a high potential for uses in food, feed, and medical industries as well as marine biotechnology. Also, it has been shown that they can produce enzymes with unique properties with many potential applications in disease control, bioremediation and new bio-product production. To our knowledge, only three marine yeasts have been identified in beaches and estuaries of Puerto Rico; Candida, Saccharomyces and Cryptococcus. The objective of this study is to isolate and identify marine yeasts associated with mangroves in Puerto Rico and determine if they produce natural compounds of possible beneficial use. Mangrove leaf-litter was collected from Playa Rosita in Lajas to isolate strains by traditional culture methods in seawater media. Samples were taken to the laboratory and cut into small pieces (approx. 0.5 cm), mostly taken for the decomposed areas of the leaf. Leaf pieces were cleaned with sterile aged seawater and then directly placed into seawater medium. Samples were incubated for 48 hours at 25 °C. As a result, from the mangrove leaves samples, we only obtained three colonies each one with different colors. These strains were observed under a microscope and all presented yeast-morphology. Furthermore, molecular characterization identified the three isolates as basidiomycete yeasts: Meyerozyma guillermondii, Kwoniella mangrovensis and Jaminaea sp.
Observations on Ascomycota saprobic community in marine sandy beaches of southwestern Pacific Coast of Mexico

POSTER B59

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Abstract

The microscopic Ascomycota that are decomposing organic substrates of plant origin in the marine intertidal sands form part of the understudied micropsamment. The isolation and identification of the culturable arenicolous mycobiota makes possible the performance of community structure analysis in different periods of time. The generated data provide evidence for future studies focused on developing conservation plans for rare and endangered fungal species and to determine how the invasive species affect autochthonous microscopic fungal diversity indigenous to the marine sandy beach environment. Furthermore, the ex situ conservation of characterized fungal isolates permits exploring potential applications in bioremediation, the discovering of new biochemicals, novel biomaterials, etc. In this study, a recent characterization of the arenicolous ascomycota community structure in Playa de Oro, Colima State, has revealed a similar pattern 20 years after a previous study. The autochthonous community of ascomycote (sensu stricto marine fungi) diversity had similar community structure as the preceding work, although the allochthonous fungal diversity showed the presence of some additional invasive species of saprobic fungi. The autochthonous marine arenicolous species Corollospora maritima was recorded with high abundance values and was present in all sampling sites along Playa de Oro. The dominant new allochthonous species was Trichoderma viride and interestingly its isolate showed fast and vigorous development in vitro.
Diversity of microscopic Ascomycota from some sandy beaches of the Mexican Pacific Coast: an incursion into bioproduct development

POSTER B60

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Abstract

In the intertidal zone of the marine beaches exists a distinctive group of Ascomycota that show adaptations to the adverse conditions of this ecotone. These fungi perform an essential function as degraders of organic matter that the waves deposit in the tideline. Fungi-based bioproduct discovery has been limited due to the lack of knowledge of fungal diversity. The aim of the study was describing the diversity of microscopic ascomycetes that inhabit the intertidal zone of the beaches in Manzanillo Bay, state of Colima, with an incursion into bioproduct development. The sampling was done in July 2018, establishing five points of sampling along the bay. To obtain the marine fungi \textit{sensu stricto} the method of incubation in humid chamber of organic remains was followed and for the marine fungi \textit{sensu lato} (facultative marine) the method of agar plate dilution was applied. All of the isolates that were obtained were characterized morphologically and molecularly and were conserved by deep freezing living material ex situ. The diversity that was recorded was characteristic of that which inhabits the beaches. The marine fungus \textit{Corollospora} sp. predominated and was present in every point of sampling. With regard to the facultative marine diversity, this was expected. Of the isolates that were recovered, we selected those that show potential for developing a bioproduct with the mycelium.
Diversity and halotolerance of endophytic fungi associated with seagrasses in Costa Rica

POSTER B61

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Abstract

Seagrasses are the only flowering plants that live submerged in the sea; seagrass meadows are among the most productive marine environments on the planet. Despite covering only 0.1% of the world's surface, they are critical carbon sinks. Seagrasses are in decline as a result of numerous anthropogenic activities worldwide, with a loss of 50% of beds globally since 1990. Because seagrass populations are in decline, it is urgent to reveal the components of their ecological network which may be critical for a healthy ecosystem. We characterized the fungal endophyte diversity of several species of seagrass from the Caribbean and Pacific coasts of Costa Rica. In addition, endophyte tolerance to high salt levels was evaluated. Culture-dependent and -independent techniques were used to assess the diversity of endophytic fungi in five species and three genera of seagrass. We isolated and identified ca. 60 fungal cultures, and detected hundreds of species using ITS2 metabarcoding. The halotolerance experiments revealed that all isolated cultures tolerate at least 40% salt concentration, and that growth rate is only slightly affected. The preliminary results of this study increase our knowledge of these fungal symbionts and potential pathogens, and may aid in conservation and restoration of these declining habitats. In addition, halotolerant isolates could be a useful source of transgenes for improved halotolerance in plants, and thus, through biotechnology, contribute to overcoming the increasing global problem of salinization of agricultural areas.
Diversity of fungi isolated from marine wood from the Bay of Fundy, Nova Scotia, Canada

POSTER B62

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Abstract

Marine fungi play an integral role in the decomposition of organic substrates, but remain understudied in coldwater intertidal habitats. Wood decay (lignicolous) marine fungi are key players in the breakdown of organic material and aid in nutrient cycling in the intertidal zone. The Bay of Fundy is home to the highest tides in the world with a 16 meter tidal range and an expansive and highly dynamic intertidal zone. The majority of the known marine fungal diversity of this region was described morphologically (direct microscopy of reproductive structures). Our study expanded the known diversity of this region through the use of culturing of fungi from intertidal wood, and ITS rDNA barcoding. 53 samples of marine inundated wood (wharf posts, driftwood) were collected between March 25th - July 6th, 2018 from 30 sites within 3 subregions (Chignecto Bay, Minas Basin, and the open Bay of Fundy), and plated onto artificial salt water agar, Czapek’s medium and Dextrose Peptone Yeast Agar. We identified 59 fungal species from marine wood (3 basidiomycetes and 56 ascomycetes). Forty of these species are new records for the Bay of Fundy and the Western Atlantic Ocean. Of the observed species, 25 and 22 were unique to the Chignecto Bay and Minas Basin regions, respectively, while 29, 8 and 8 species were unique to intertidal attached, intertidal loose and driftwood substrates, respectively. The marine fungal diversity of Bay of Fundy marine wood exhibits possible regional and wood substrate specific distributions.
Polyextremotolerant fungi, Trebouxioid algae, and Methylobacterium bacteria: a Symbiotic Trifecta of Biological Soil Crusts

POSTER B63

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Abstract

Biological soil crusts (BSCs) are complex microbial biofilms found in xeric soils that can withstand a wide range of extreme conditions including: heat, freezing, desiccation, osmolarity, UV, oligotrophic conditions, and heavy metals. Organisms that are most commonly found in BSCs are fungi, algae, bacteria, lichens, and mosses. Microbial species of particular interest to our research goals are polyextremotolerant fungi from the order Chaetothyriales, as well as algae from the class Trebouxiophyceae and bacteria belonging to Methylobacterium spp. Unique features of these organisms make them intriguing to study in isolation, but may also provide insight into the development of fungal-algal and fungal-bacterial interactions. These microbes are closely related to lichen-forming microbes, to the extent that they share similar traits while not strictly adopting the lichen lifestyle. Accordingly, we propose that these members of the larger BSC community interact in a mutualistic fashion similar to that of lichens, and, that observation of these interactions will reveal clues about the nature of the microbial communication that underlies the viability of BSCs. We have used culture-dependent and independent methods to describe microbial interactions in a BSC from a semi-arid sand dune ecosystem. Current efforts are focused on integrating microbiome, physiological, and mixed-culture methods to understand the functional interactions that enable the formation and maintenance of these microbial interactions.
Just Deserts? Exploring the Diversity of Melanized Fungi in Rocks and Biological Soil Crusts

POSTER B64

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Abstract

Desert drylands are extreme environments and inhabiting organisms of these ecosystems must endure high UV irradiation, temperature fluctuations, aridity and oligotrophy. Biological soil crusts (BSC’s) are microbial assemblages comprised of bacteria, fungi, algae and bryophytes. Lichen BSCs are slow growing, long-lived crusts and can be functionally differentiated by their photobiont partner which can either be cyanobacteria (Cyano-Lichen Crusts; CLC) or algae (Green Algal Lichen Crusts; GLC). The fungal component of these crusts remains understudied and our work has focused on melanized fungi found within. Dothideomycetes and Chaetothyriales (Ascomycota) melanized fungi can be isolated from water limited environments including deserts, glaciers, hypersaline and marine systems, and rock surfaces.

Using culture dependent and independent approaches on CLC and GLC samples from Mojave and Colorado Deserts (USA), we isolated melanized fungi from the genera Knufia, Coniosporium, Sarcinomyces, Didymella, and Acremonium. Amplicon sequencing found high relative abundance of melanized fungi in CLC as compared to GLC or Light Algal crusts. Serial dilutions of BSC material cultured on minimal oligotrophic media and antibiotics to develop a culture collection of melanized fungi. Internal Transcribed Spacer and whole genome sequencing of isolates revealed multiple new species. Comparative genomics with related melanized yeasts isolated from Antarctic endolithic communities and marine environments allowed comparison between fungi from hot and cold extremes. We are integrated of phylogenetic, comparative genomics and ecological context to better understand evolutionary history and the functions or processes promoting melanized fungal success in the extremes.
Diversity on the continental edge: Taxonomic investigations into the poorly studied corticioid fungi at the Boston Harbor Islands reveal undescribed species and new reports for North America

POSTER B65

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Abstract

Only 1 to 2% of the estimated 5–10 million species of fungi are described. Focused collecting efforts and molecular phylogenetic studies are severely lacking for many groups of fungi, such as corticioid fungi—or crusts. Corticioid fungi form a non-monophyletic group of Basidiomycota with resupinate, effused morphologies and are spread across almost all orders in the Agaricomycetes. Their unremarkable and often cryptic fruiting bodies have severely limited the number of people properly trained to identify these fungi. This is unfortunate: crusts are vital for forest ecosystem functioning, both as saprotrophs and ectomycorrhizal symbionts, especially in coniferous forests. Since December 2012, we have conducted a fungal inventory at the Boston Harbor Islands National Recreation Area (BHI) in Massachusetts. We made over 900 collections, of which 313 have been identified mostly through ITS rDNA barcoding, motivating in-depth studies of the remaining fungi. About 10% of collections are crust fungi. Through focused taxonomic investigations on the unidentified crusts, we documented dozens of species, added newly generated ribosomal DNA sequences to GenBank, documented new reports for North America, and are in the process of describing new species of Atheliales, Atheliaceae and Lyomyces (Hymenochaetales, Schizoporaceae). Future work includes an integrative taxonomic revision of the genus Athelia and the identification of remaining corticioid fungi from the ecologically diverse BHI at the edge of the continent. We also aim at making information on corticioid fungi more broadly accessible by making species descriptions and macro- and microscopic photographs available to the public through the website crustfungi.com.
The Canadian Collection of Fungal Cultures (DAOMC) and the National Fungal Identification Service of Canada (NFIS): at your service

POSTER B66

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Abstract

The Canadian Collection of Fungal Cultures (DAOMC/CCFC) and the National Fungal Identification Service (NFIS), at the Ottawa Research and Development Centre, work together to support the fungal research community. The facilities are supported by expert taxonomists in most major taxonomic groups whose research is mainly concentrated on solving agricultural problems.

DAOMC/CCFC is Canada’s largest source of authenticated fungal isolates. It is an internationally recognized culture collection maintaining ~20,000 cultures, representing >4000 species, including many ex-type. The primary focus is plant pathogenic and mycotoxigenic fungi that may have potential as invasive species to Canada, and potentially beneficial fungi for agricultural productivity. It is the primary Canadian repository for research strains, provides pure cultures to researchers in agriculture, forestry, medicine, private industry and biotechnology. The collection has been databased in an application that provides standards-compliant information management for collection records. DNA barcoding was performed on 4406 specimens from the CCFC, with the goal of barcoding for all living cultures in the collection. Partial/full genome sequences will also be generated for 575 specimens.

NFIS supports scientists, industry, and academia by providing identification of pure cultures. Multiple gene loci sequencing and microscopic observations are combined, with local taxonomic expertise to identify to the species level. The service focuses primarily on agriculturally relevant fungi. The combination of the two services is a valuable resource for fungal ecology, genetics and systematics allowing us to increase knowledge of the DAOMC reference collection and providing well supported identifications to the fungal research community.
Developing mycological educational resources for biology and environmental science teachers and students

POSTER B67

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Abstract

Middle and high school biology and environmental science teachers usually have limited time to teach about fungi as isolated taxonomic units and are required to be compliant with national and state science standards. In this presentation, we describe the partnership between a science education researcher, a middle school teacher, and a mycologist that led to the teaching of a unit on fungi in an 8th grade science class. Through the use of lesson components such as case studies and graphic organizers, students used the 5E model of learning to gain authentic scientific experience by drawing, observing and dissecting fungal specimens. Students demonstrated a high degree of enthusiasm during the unit which utilized progressive pedagogical strategies such as student-centered, inquiry-based, and collaborative learning. Summative assessments showed that students gained a working knowledge of fungal characteristics and their place in the ecosystem. While the unit was taught before a state standards-based unit on disease, fungi are relatively underrepresented in the national Next Generation Science Standards. More activities that promote and strengthen collaboration among scientists, students, and teachers could lead to an increase in the importance of mycology as perceived by the public and society. Guidelines and challenges for developing collaborative and interactive partnerships between mycologists and teachers are discussed further in this presentation.
Mycology at Itasca - Fungus forays for credit, since 1908

POSTER B68

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Abstract

At the edge of the boreal biome in Minnesota in Itasca State Park, one can climb a fire tower and get above the towering old growth pines. Facing west into wilderness, the coniferous transition to deciduous forest is apparent, and if it were not eclipsed by the ridge along the Laurentian Divide, one could see into the prairie and ancient Lake Agassiz. Itasca Biological Station sits at this crossroads, within Itasca State Park and within an hour of three biomes.

Itasca Station has been in operation since 1908 - mycologists were there from the beginning, starting with Arthur Ruggles and Edward Freeman. Over 120 years, mycologists such as Christiansen, French, Gilbertson, Pfister, Steward, and McGlaughlin have forayed and taught at Itasca. Forestry students in the Roosevelt era came for the old growth - the mycologists, along with a flood of other biology students, also came for old growth, but stayed for the headwaters location on the Mississippi River, the lakeside setting, and the quick access to three major U.S. biomes.

As of 2019, Itasca is offering Field Mycology in parallel with Field Microbiology. The classic morphology-based field ID in the mycology course will enable students the opportunity to learn, hands-on, about fungi in this diverse environment. The DNA-based tools such as MiniSeq are also enabling faster turnaround for community-level data and genomics fueled by microbial efforts in bacterial and fungal realms. This, we believe, can link molecular tools to morphological techniques, taught in a location that links the past to the future.
Little evidence of antagonistic selection in the evolutionary strata of fungal mating-type chromosomes (*Microbotryum lychnidis-dioicae*)

**POSTER B69**

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**Abstract**

Recombination suppression on sex chromosomes often extends in a stepwise manner, generating evolutionary strata of differentiation between sex chromosomes. Sexual antagonism is a widely accepted explanation for evolutionary strata, postulating that sets of genes beneficial in only one sex are successively linked to the sex-determining locus. The anther-smut fungus *Microbotryum lychnidis-dioicae* has mating-type chromosomes with evolutionary strata, only some of which link mating-type genes. Male and female roles are non-existent in this fungus, but mating-type antagonistic selection can also generate evolutionary strata, although the life cycle of the fungus suggests it should be restricted to few traits. Here, we tested the hypothesis that mating-type antagonism may have triggered recombination suppression beyond mating-type genes in *Microbotryum* by searching for footprints of antagonistic selection in evolutionary strata not linking mating-type loci. We found that these evolutionary strata (i) were not enriched in genes upregulated in the haploid phase, where cells are of alternative mating types, (ii) carried no gene differentially expressed between mating types, and (iii) carried no genes displaying footprints of specialization in terms of protein sequences (dN/dS) between mating types after recommended filtering. Without filtering, eleven genes showed signs of positive selection in the strata not linking mating-type genes, which constituted an enrichment compared to autosomes, but their functions were not obviously involved in antagonistic selection. Thus, we found no strong evidence that antagonistic selection has contributed to extending recombination suppression beyond mating-type genes. Alternative hypotheses should therefore be explored to improve our understanding of the sex-related chromosome evolution.
Genetic Diversity of the Mating-Type Pheromone Receptors in Genus *Rhizopogon*

POSTER B70

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Abstract

The genus *Rhizopogon* are ectomycorrhizal (ECM) fungi that are globally distributed with host trees of the family Pinaceae. *Rhizopogon* species have a very high degree of ECM host specificity and many species will associate with only a single host tree genus or species. There are currently five recognized subgenera of *Rhizopogon* and these subgenera possess a range of host specificity from obligate association with a single host genus to generalist association with several host genera. Despite the clear ecological significance of these fungi in both natural and managed forests, very little is known regarding their population structure and reproductive strategies. A few studies have performed landscape scale comparisons of closely related species in natural stands of *Pseudotsuga* and *Pinus* host trees. Recent studies have also investigated the organization and diversity of mating-type loci from individuals of the sister species *R. vinicolor* and *R. vesiculosus* in *Rhizopogon* subgenus *Villosuli*. In this study we expand the study of *Rhizopogon* reproductive strategies. To do so we have characterized the mating-type loci of 6 additional individuals of the sister species *R. vinicolor* and *R. vesiculosus* and another 8 individuals from species spanning all five *Rhizopogon* subgenera. Our results show shared structural traits and content between the *B*-locus mating-type pheromone receptors of many species of *Rhizopogon*, suggesting that *Rhizopogon* species have developed similar reproductive strategies in response to similar selective pressures.
Whole-genome sequencing and assembly to discover candidate SSR loci for population genetic analysis of the spruce bud blight pathogen *Gemmamyces piceae* (Melanommataceae)

POSTER B71

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Abstract

*Gemmamyces piceae* causes bud blight disease of *Picea* species in Europe and China. It was first discovered in Alaska in 2016 and by 2017 Gemmamyces bud blight was recorded at over 31 locations in South Central and Interior Alaska. The pathogen is of concern because 90% of forest land in Alaska is boreal forest dominated by *Picea* species and the fungus causes reduced growth, dieback and in Europe even mortality. Two isolates were subjected to whole-genome sequencing with 150 bp paired-end reads yielding 15 Gb data at >100X coverage. The isolate with more sequence data was used for genome assembly. Reads were quality trimmed using Trimmomatic and *de novo* assembly was performed using ABySS with a k-mer pair span of 64. Simple Sequence Repeats (SSRs) were mined using Msat Commander. A total of 528 candidate SSR loci were identified for which suitable primer sequence were designed. Motifs sought were tri-, tetra-, penta-, and hexa-nucleotide repeats, with shorter repeats being more abundant than longer repeats (239 were tri-nucleotide repeats and 61 were hexa-nucleotide repeats). One candidate primer for each locus was designed for indirect fluorescent labeling by addition of a short CAG-sequence that was complementary to a third primer. On the alternate primer, a GTTT sequence was added to create a poly(A) tail that reduces stutter peak formation. A selection of candidate primers will be evaluated for ability to detect polymorphism within populations from Alaska and the Czech Republic for subsequent applications to characterize the population structure and migration patterns.
Evolution of the mating type locus in Mucoromycotina

POSTER B72

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Abstract

Changes to developmental gene expression drive morphological evolution across eukaryotic lineages. The cis-regulatory elements and transcription factors that control differential gene expression play an important role in the early stages of development from determining cell identity to influencing body plans. The regulators of development have been studied across eukaryotes from Hox genes in animals to MADS-box genes in plants. In fungi, the mating type locus (MAT) harbors genes involved in sexual development. The bipolar mating system in Mucoromycotina (Phylum: Mucoromycota) is exemplified by a single MAT locus which encodes idiomorphical alleles. MAT alleles designated plus (+) have a High Mobility Group-domain encoding gene SexP and minus (-) alleles a SexM gene. Evidence from a subset of Mucoromycotina suggests the mating type locus is syntenically conserved, where the HMG-domain genes are flanked by a triose phosphate transporter and RNA helicase gene. Our analysis of 144 Mucoromycotina genomes finds that gene content and MAT locus order are conserved. We find that MAT loci are more compact in species with observed sexual reproduction than those where it has not been seen, suggesting that relaxed selection and drift may be occurring. In some species MAT loci have gained additional genes within the locus in a mating-type specific manner. We generated mating-type specific phylogenies for species with known mating pairs and suggest that SexP locus has an ancient origin as the topology is consistent with the species phylogeny in contrast to SexM.
Formation of natural hybrids between *Puccinia hordei* and *Uromyces scillarium*

**POSTER B73**

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**Abstract**

*Puccinia hordei* is a heteroecious macrocyclic rust fungus that causes leaf rust of barley. The uredinial and telial stages of *P. hordei* are found on *Hordeum* spp. and the pycnial and aecial stages are found on *Ornithogalum* spp. *Uromyces scillarium* is a microcyclic rust fungus, producing only telia and basidia on *Ornithogalum* spp. Telia of *P. hordei* were induced to germinate and used to infect *O. eigii* plants in a greenhouse. It was observed that *P. hordei* infections near natural occurring infections of *U. scillarium* produced only aecia. Aeciospores were collected from these “near” aecial cups and used to infect barley. Teliospores derived from the “near” aecia had morphological characteristics (teliospore area and percentage of mesospores) that were intermediate between *P. hordei* and *U. scillarium*. *P. hordei* infections of *O. eigii* “far” from *U. scillarium* infections formed normal pycnia and aecia and were used as controls. DNA sequence analysis of a 1.5kb segment of the gene encoding the elongation factor 1-alpha (EF1a) was performed. Collections of *P. hordei* and *U. scillarium* each had distinct EF1a sequences while the collections that originated from the “near” infections contained both EF1a sequence types (EF1a-Ph, EF1a-Us). Selected isolates originating from the “near” aecia were selfed. The resulting progeny exhibited two distinct classes: “hybrid” type with intermediate teliospore morphology and both EF1a sequence types (EF1a-Ph, EF1a-Us); “Ph” type with teliospore morphology and only the Ph-EF1a sequence type. These results indicate that natural hybridization occurs between *P. hordei* and *U. scillarium*. 
Genetic structure of contemporary populations of the boxwood blight pathogen in the USA

POSTER B74

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Abstract

\textit{Calonectria pseuodonaviculata (Cps)} is currently the most devastating pathogen of boxwood (\textit{Buxus} spp.) worldwide. \textit{Cps} can also infect other members of the Buxaceae, namely, pachysandra (\textit{Pachysandra procumbens, P. terminalis}) and sweet box (\textit{Sarcococca} spp.). In the U.S. the disease was detected for the first time in North Carolina and Connecticut in 2012 and is now present in 28 states. A previous study reported that \textit{Cps} residing in the U.S. prior to 2014 had a clonal population structure, and only the MAT1-2 mating type was present. However, the genetic structure of contemporary populations of this pathogen remains unknown. In the present study, we set out to estimate genetic diversity and gene flow in U.S. populations of \textit{Cps}, and to assess the importance of sexual reproduction. We used Illumina technology to sequence 11 SSR loci and the MAT1 locus from 176 isolates of \textit{Cps}, sampled from 2014 to 2019 across 18 states. Preliminary data (10% of isolates examined) showed the prevalence of a single SSR genotype, which was also the most common genotype in the U.S. prior to 2014. A new SSR genotype was identified from a \textit{Cps} isolate from Pennsylvania, which differed from the predominant genotype by a single SSR allele.
Population genomics in *Macrophomina phaseolina* reveals geographic structure and potential temperature adaptation among the US, Puerto Rico, and Colombia

**POSTER B75**

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**Abstract**

*Macrophomina phaseolina* is an important pathogen of crops worldwide. Charcoal rot caused by *M. phaseolina* can significantly reduce yield and seed quality in soybean and dry bean mainly in tropical and subtropical regions. Little information is available on the population structure of *M. phaseolina*. Genomes of 96 *M. phaseolina* isolates from 13 states across the US, Puerto Rico, and Colombia, isolated from various hosts were sequenced to determine whether populations are structured by host or geographic origin. Sequencing was performed on an Illumina HiSeq 4000 with 150 bp paired-end reads to an average depth of 23X. Minimum spanning network analysis (MSN) based on Provesti’s genetic distance indicated isolates exhibit a clonal genetic structure, which can be supported by the biology of *M. phaseolina* since a sexual stage has not been identified. Interestingly, MSN and discriminant analysis of principal components revealed clustering of Puerto Rican and Colombian isolates from dry bean, while isolates from the US regardless dry bean or soybean were assigned to a separate cluster and exhibited lower diversity. The clustering and the higher genetic diversity in isolates from Puerto Rico and Colombia indicated the possibility of population differentiation. To investigate temperature adaptation, mycelial growth at 15°C and 35°C was measured and some isolates from the states of Michigan, Wisconsin and Minnesota grew faster at 15°C than isolates from southern states. Genome-wide differentiation between proposed populations is being investigated, as well as identification of candidate genes that are associated to cold adaptation.
Genetic Diversity and Population Structure of *Sporisorium ellisii* (Ustilaginaceae) within and among three populations in the Eastern United States (New Jersey, Pennsylvania and Ohio)

POSTER B76

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Abstract

The smut fungus *Sporisorium ellisii* (G. Winter) M. Piepenbr. on its common U.S. host, *Andropogon virginicus* (Broomsedge) has received little attention beyond taxonomic placement in its current genus and mycogeographic citations. This obligate parasite, once successfully infective, produces sori which replace the inflorescences of its host as is typical of most smut fungi. It does not, however, generate sporidia upon the germination of teliospores on PDA, water agar or host extract-spiked agar, but instead produces a slow-growing, limited mycelium. In culture on PDA, the mycelium darkens and ceases growth after about 10 days at 25°C.

Three populations of this parasite were located in New Jersey, Pennsylvania and Ohio (the latter, focal). From infected plants collected along multiple, parallel transect lines 50m long, spores were collected, cold-stored for >2 months, surface-sterilized with dilute bleach and cultured on PDA with streptomycin (0.06g/l). Mycelia grown from single spore cultures were inoculated into PD broth and within a week, homogenized in lysis buffer and chloroform-isoamyl extracted. The genomic DNA from ~20 isolates/population was then run against 18 ISSR primers and 10 ScoT primers that reliably produced clear bands. The ISSR primers yielded 154 useful bands (ave. of 8.6 bands/primer) ranging from 400-2000 bps. The ScoT primer work is ongoing. For the ISSR primers, the PIC/primer values ranged from about 0.1 – 0.4. Via AMOVA, within population variance is 79% and among-population variance is 21%. A UPGMA dendrogram and correlation of genetic distance with geographic distance (via Mantel tests) will be presented.
Megaphylogeny of mushroom-forming fungi helps to understand evolutionary patterns of complex multicellular structures

POSTER B77

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Abstract

Mushroom forming fungi (Agaricomycetes) is one of the biggest classes (>20,000 species) in the fungal kingdom with diverse morphologies and various ecological roles, yet its macro-evolutionary history is poorly known. To examine its evolution, we inferred a multigene phylogeny of the Agaricomycetes consisting of 5,284 species and three loci (nrLSU, RPB2 and ef1-a), combined with a phylogenomic backbone of 104 species and chronograms were estimated by applying temporal information of eight fungal fossils. First, we estimated the character state independent diversification rates using BAMM. We found an acceleration in diversification of species that started in the early Jurassic, coinciding with the spread of coniferous forest and emergence of pileate-stipitate fruiting bodies. Signs for a mass extinction were detected (BAMM and TESS analyses) in the late Jurassic, but not at the Cretaceous-Tertiary boundary, when a mass extinction event affected wide range of animal and plants species. The broad macro-evolutionary pattern mentioned above consists of several (>85) lineage-specific shifts in diversification rate suggesting a complex evolutionary history of mushroom forming fungi. This pattern could be shaped by several key morphological innovations; therefore, we inferred the character state dependent diversification rates related with fruiting bodies and found that the presence of a cap, increased hymenophore surface and the presence of veil tissues could have spurred lineage diversification.
Conflict as a motor for evolutionary change: insights from the fungal genomes

TUES 1

Hanna Johannesson
Department of Forest Mycology and Pathology, Swedish University of Agricultural Sciences, Uppsala, Sweden

Abstract

In fungi, meiotic drive is observed as spore killing. In Neurospora, it is apparent from the abortion of four of eight spores in the ascus, while in the pseudohomothallic Podospora it is characterized by the abortion of two of the four spores. In our laboratory, we use a combination of genetics, genomics, and molecular evolution approaches to investigate the causes and consequences of spore killing in these two systems. We find that the genetic bases of spore killing vary from large multigene loci to single genes. We see that in Neurospora, only one spore killer is found in each species, while in Podospora multiple drive elements are found to coexist in the same population. In both Neurospora and Podospora, spore killer genes are being introgressed between species, and while the multigene loci have a significant impact on chromosome structure, the single gene drivers are dispersing by duplication within genomes.
Mycelium Materials: Developing Mylo™ leather at Bolt Threads

TUES 2

Andrea Bruce
Bolt Threads, Emeryville, CA, USA

Abstract

Bolt Threads is a California-based biotech creating what we believe are the next generation of nature-inspired materials. The company launched in 2009 synthesizing spider silk for textiles and has recently introduced its second biomaterial: Mylo™ leather made from mycelium. I was hired to help develop Mylo™ leather as Senior Research Associate during fall 2018, about one month before my master’s thesis defense. Having recently transitioned from studying mycology in academia to working with mycology in industry, I will share my experience applying and interviewing for jobs, in addition to discussing my current role at Bolt and how my training in mycology got me there.
Mycology at the CDC

TUES 3

Anastasia Litvintseva

Centers for Disease Control and Prevention, Atlanta, USA

Abstract

As a team lead of the Fungal Research Team at the Mycotic Diseases Branch, CDC, I lead a group of investigators working to improve the diagnosis, treatment, prevention and control of fungal diseases. Our group works with domestic and international partners to understand the ecology and epidemiology of fungal infections, provide laboratory support to outbreak investigations and works with epidemiology teams to address public health problems related to fungal infections. Our team has been actively involved in the response to newly emerging multidrug resistant *Candida auris*. Specifically, our team was the first to use a whole genome sequencing approach to demonstrate the recent independent emergence of *C. auris* in four different geographic areas. In addition, we provide laboratory support to fungal outbreak investigations and are actively involved in the development of novel methodologies for detection and genotyping of fungi to understand potential sources and transmission modes of fungal infections. In my presentation I will discuss the current projects in our group.
Mycology in a mushroom spawn company

TUES 4

Andrii Gryganskyi

LF Lambert Spawn Co., Coatesville, USA

Abstract

Beginning. I graduated from T. Shevchenko Kyiv State University in 1991. The same year I started graduate study in M. Kholodny Institute of Botany, National Academy of Sciences of Ukraine. During my graduate study, I was also closely involved in the development of commercial mushroom growing in Ukraine, collaborating with and consulting with many mushroom farms. During this time, I also started my collaboration with European researchers and the mushroom industry abroad, which resulted in several grants, scholarships, and visits to the universities, research centers, and mushroom farms in Europe.

Duke University. I joined Duke University in January 2008. Primarily I was doing my research for AFToL, focusing on early diverging terrestrial fungi with emphasis on Entomophthoromycotina. That same year I also joined the lab of Joseph Heitman studying sex genes in Rhizopus.

Lambert Spawn company. I was hired by LF Lambert Spawn Co. in 2014 as a researcher/molecular biologist. My role in the company is to create a new commercial strain of brown agarics, with the aim of developing a white strain as well. My work includes the generation of suitable breeding material (homokaryons), crossing them, and evaluating them on several aspects important for cultivation. This work involves molecular, genomics and bioinformatic skills. For example, we sequenced 16 genomes of homo- and heterokaryons, including our commercial strains and most promising hybrids. We are in the experimental stage in designated mushroom farms now.
**Mycology at the US Forest Service**

**TUES 5**

_Daniel Lindner_
USDA Forest Service, Madison, USA

**Abstract**

Daniel Lindner has been a research mycologist at the US Forest Service’s Center for Forest Mycology Research since 2003. His research aims to understand how humans affect fungal communities, and how these changes can in turn affect larger ecosystem processes. Daniel’s research has focused on forest management techniques and their influence on fungal communities and carbon sequestration, as well as the interactions between fungi (both pathogenic and beneficial) and wildlife. Daniel has studied the relationships between fungi and the federally endangered Red Cockaded Woodpecker, as well the interactions between insectivorous bats and the fungus *Pseudogymnoascus destructans*, which causes the devastating disease known as White-Nose Syndrome of bats. Daniel received his Ph.D. from the University of Wisconsin-Madison, Department of Plant Pathology in 2001. His Ph.D. research examined the effects of forest management on wood-inhabiting fungal communities in the upper Midwest. Following his Ph.D., Daniel lived in Uppsala, Sweden where he conducted post-doctoral work investigating DNA-based methods for identifying fungi associated with complex environmental substrates.
Museum mycology

TUES 6

Bryn T. M. Dentinger

University of Utah, Salt Lake City, USA

Abstract

Museums provide career options distinct from academia and industry. While maintaining an independent identity, they are sometimes associated with academic institutions, sometimes government agencies, and sometimes private industry. In each case, the responsibilities of museum staff can be somewhat different than traditional academic staff, particularly with regards to specimen curation and public engagement. In this presentation, I will share my experiences working with four different museums in three countries, both academic and government, that span my career from graduate school to my current position as a curator with a cross-appointment in a university department.
Thinking again about the fitness of filamentous fungi

TUES 7

Anne Pringle
University of Wisconsin-Madison, Madison, USA

Abstract

In 2002 John Taylor and I published an analysis of the fitness metrics used to gauge evolution among filamentous fungi. We suggested that focusing on a single measure of fitness can be appropriate and particularly if the metric is contextualized by an understanding of underlying trade-offs. Curious to know how our work has been used in the last fifteen years, I analyzed the literature citing our original article to understand how often the article is used to justify a particular fitness metric, whether some fitness metrics are more popular than others, and if the article has been used to extend mycologists’ nascent philosophy of fitness. Often, the article is used to justify numbers of spores as a fitness metric. Surprisingly, the paper is also used to support various claims of fungal life histories as “complicated”. But emerging within the citing literature are different unsolved problems. The ecological relevance of phenotypes ranging from color and shape to secondary metabolite production remains obscure; even with clear definitions of fitness, identifying the selective forces driving adaptation and judging whether a trait is adaptive remain daunting challenges.
Teaching with Taylor - a short history of two mycology courses and the Mendocino foray

TUES 8

Thomas Bruns
University of California, Berkeley, USA

Abstract

John Taylor taught the Biology of the Fungi course at Berkeley every other year since the early 1980s through 2016. This was a 15-week, comprehensive, survey course on the fungi that included two, three-hour labs/week. The content included slime molds, Oomycota, a few other fungal-like eukaryotes, and of course the true fungi. Since 2002 I had the pleasure of co-teaching this course with him, and in 2013 we developed a new, non-majors course together: Fungi, History, and Society. Both courses had three weekend fieldtrips designed to broaden the educational experience and build camaraderie among the students. One of these fieldtrips, the Mendocino foray, was started by Harry Theirs (SF State Univ.) and Ken Wells (UC Davis), and it predated the Berkeley courses. John Taylor initiated Berkeley’s participation into this foray in the early 80s, and he became the de facto organizer of it for three decades. Many undergraduates and graduate students at SFSU, UC Davis, and Berkeley were first exposed to the mushroom diversity at this foray. Participation has expanded over the years, and last year the foray included students and professors from seven universities. Species lists have been kept for this foray since 1992. These lists show dramatic variation between years but also document an increase in our ability to identify species as the collective knowledge of the participants has expanded.
On fungal pathogenesis: an homage to John Taylor

TUES 9

Joseph Heitman
Duke University, Durham, USA

Abstract

The diversity of the Fungal Kingdom is staggering, with as many as 2.2 to 3.8 million species, and maybe more! A minority of fungi have evolved into devastating pathogens of plants and animals, including humans. How pathogens are related to saprobic ancestors is a central question. The ways that we think about the broader organization of the Fungal Kingdom, species boundaries, specialization as saprobes evolve to pathogens, and genetic exchange within populations has been shaped, framed, and influenced by studies from John Taylor and colleagues. This talk will focus on recent studies on genomes and evolutionary transitions in the Cryptococcus/Kwoniella species complex that includes a monophyletic group of human pathogens embedded within a broader group of saprobic species, many of which have only recently been identified, and are being named. These studies can provide some general insights into species identification, transitions in modes of sexual reproduction, genome evolution and chromosome and karyotype changes, and transitions from saprobic to pathogenic potential.
**Missing fossils and strategies to fill the great gaps in the geological record of fungi**

**TUES 10**

Mary Berbee  
Univ. British Columbia, Vancouver, Canada

**Abstract**

Geological age estimates draw on fossils, phylogenies, ecological considerations, and time estimates from molecular dating. Age estimates for some land plant and animal clades are increasingly reliable because they are constrained by multiple lines of evidence. In contrast, great uncertainty surrounds age estimates for fungi. Interpretation of some fungal fossils from Rhynie Chert (417 Ma) are consistent with morphology, host associations, and recurring appearances through geological time. However, the fungal lineages should be far older, given even the most conservative molecular dating (including ours). Tracking fungi further back requires other evidence. Molecular genetic evidence of signaling interactions or enzymes and substrates show that plant-fungal interactions likely began with algae. Among Dikarya, interpretation of 417 Ma fossils as ascomycetes is made puzzling by a subsequent 80 million-year gap before the first Basidiomycota fossils and by a 200 million-year gap before Ascomycota (Pezizomycotina) spores appear in the fossil record. Solving the puzzle could include new discoveries of Carboniferous fungi. Analysis of dispersed fossils may show whether patterns of Mesozoic diversity are consistent with diversification that could have begun 200 Ma earlier. Gaps in fossil records may be artifacts of overestimates of ages from molecular dating or merely the inevitable consequence of hundreds of millions of years of missing or uninterpretable fossil data. Either way, concerted efforts to find and interpret fossil data and to further analyze genomic data will contribute to illuminating the parts played by fungi in the story of the biology of early colonization of land.
What can we learn about evolution of symbioses from the partnerships between fungi and bacteria?

TUES 11

Teresa Pawlowska
Cornell University, Ithaca, USA

Abstract

Despite their narrow phylogenetic partner ranges, fungal-bacterial symbioses are diverse in terms of function, evolutionary history and antiquity. Because of these features, partnerships between early divergent fungi in the phylum Mucoromycota and endobacteria representing Betaproteobacteria and Mollicutes provide excellent study systems for testing theoretical models that explain establishment and evolutionary stability of symbiotic associations. For example, we used the early Devonian symbiosis between Glomeromycotina and 'Candidatus Glomeribacter gigasporarum' to challenge the model of degenerative genome contraction in vertically transmitted endobacteria and demonstrated that the genomes of such bacteria can evolve nondegenerately. In turn, the symbiosis between Glomeromycotina and 'Candidatus Moeniiplasma glomeromycotorum' illustrated that heritable symbioses can evolve as a consequence of trans-kingdom host switches by horizontally transmitted symbionts. Lastly, the symbiosis between Rhizopus microsporus (Mucoromycotina) and endofungal Burkholderia provided empirical support for evolution of mutualisms through hosts becoming addicted to antagonistic symbionts while these symbionts assume control over their own vertical transmission. The Rhizopus-Burkholderia symbiosis is now also yielding insights into evolutionary changes that occur in the host to accommodate microbial symbionts, which is an emerging theme in the symbiosis research.
Twenty years of genealogical concordance phylogenetic species recognition in Fungi: How did we get here? And where are we going?

TUES 12

David Geiser
Penn State University, University Park, PA, USA

Abstract

This talk will be a reflection on genealogical concordance phylogenetic species recognition (GCPSR), a multilocus sequence-based approach to recognizing species in Fungi. This approach was first described in detail by John Taylor et al. 2000 (*Fungal Genetics and Biology* 31: 23-32). Reflecting its influence on the field, this paper is the most-cited publication in that journal’s history, and it continues to amass citations at rates of >90 per year. GCPSR was the result of innovative approaches employed in the Taylor lab in the 1990s, specifically with the discovery that the Valley Fever pathogen *Coccidioides immitis* showed clear evidence of a species boundary aligned with geography. I will briefly summarize the origins and rationale associated with GCPSR, and using a few examples of later studies where the approach was employed, attempt to provide a critical reckoning of its strengths and weaknesses in the context of real organisms and real data. I will conclude by highlighting a phylogenomic picture of fungal species presented recently by Taylor, which reveal populations of interbreeding individuals within GCPSR-diagnosed species, and a possible genetic diversity approach to quantifying their status. I will then attempt to reconcile the varying outcomes from GCPSR analysis with the practical need to recognize species in Fungi.
Opening the “black box” of demography: what is killing seeds?

TUES 13

Bitty Roy¹, Hunter Mackin¹, Tiffany Thornton¹, Kayla Evens¹, Devin Dunwiddie¹, Allison R Ludden¹, Holden Jones², Zoe Wender², Krista L. McGuire¹

¹University of Oregon, Eugene, USA. ²Lewis and Clark College, Portland, USA

Abstract

Studies of plant demography typically measure host reproduction and survival, including production of seedlings. Many more seeds are produced than seedlings emerge, so what kills the seeds? To begin addressing this question, we combined germination tests and analysis of pathogens present for two native grass species, *Festuca roemeri* and *Danthonia californica* from a demographic study of multiple populations across a climate gradient. The sites differed in characteristics such as plant density, latitude, precipitation and temperature and could be grouped into three regions: Southern Oregon, the Willamette Valley, and the Puget Trough. During germination testing we visually scored presence of common genera on the exterior of the seeds. Seeds that did not germinate were split into two groups: one was cultured for fungi, followed by Sanger sequencing; the other was prepped for community analysis using Illumina sequencing. We expected that the environmental drivers would influence seed germination, fungal species on the exterior of seeds, and pathogen abundance and diversity. In addition to strong climate signals indicating sensitivity to these conditions, we saw regional differences, suggesting dispersal limitation. We also found that in *Danthonia*, cleistogamous seeds (which are enclosed in the mother) had fewer pathogens than chasmogamous seeds (which are exposed to wind and air). As we’ve illustrated, a broader toolset for studying seed pathogens is now available to assist in unearthing the details of demographic studies.
Environmental factors affecting selenite reduction mechanisms by Ascomycete fungi

TUES 14

Jacqueline Mejia¹, Mary Sabuda¹, Carla Rosenfeld²

¹University of Minnesota, Minneapolis, USA. ²Northwestern University, Evanston, USA

Abstract

Selenium (Se) pollution is a global problem because, like mercury, this element bioaccumulates and reaches toxic levels that are detrimental to aquatic and terrestrial ecosystems. Se pollution is observed due to weathering of phosphorus rocks, black shales, volcanic rocks, copper ores and coal, which are associated with Se in the environment. Yet, hazardous Se concentrations are only detected when anthropogenic activities such as coal combustion, metal refining and mining take place. Se toxicity is mainly caused by two oxidized forms of Se, selenite and selenate. These oxyanions can be reduced by various fungal and bacterial species to less toxic phases such as elemental Se or volatile selenide compounds. However, the biological mechanisms involved in Se reduction and the effect of environmental conditions on these mechanisms is unknown for fungi. This project uses batch laboratory experiments combined with geochemical assays and RNA sequencing transcriptomics to elucidate pathways and mechanisms involved in the reduction of selenite by two Ascomycete fungi: Alternaria alternata SRC1lrK2f and Paraconiothyrium sporulosum AP3s5-JAC2a. We hypothesize that fungal Se tolerance, reduction rates, products, and metabolic pathways vary depending on: initial selenite concentration, fungal species and environmental conditions (e.g., organic carbon source and sulfate concentrations). Understanding fungal Se reduction mechanisms will allow us to determine optimal conditions for the conversion of toxic Se oxyanions to less toxic elemental Se particles that can be recycled for various biotechnological applications such as fertilizers, glass, pigments, pesticides, semiconductors and sensors. Overall, treating Se-contaminated environments is important for ensuring healthy ecosystems around the world.
HURRICANE DISTURBANCE AFFECTS FUNGAL COMMUNITIES AND MYCORRHIZAL NETWORK IN A NEOTROPICAL FOREST

TUES 15

Julieta Alvarez-Manjarrez¹, Mohammad Bahram², Sergei Polme³, Roberto Garibay-Orijel¹

¹Instituto de Biología, Ciudad de Mexico, Mexico. ²Swedish University of Agricultural Sciences, Uppsala, Sweden. ³Natural History Museum, Tartu, Estonia

Abstract

Hurricanes will increase in number and intensity while ocean water temperature gets warmer. These events produce damage in vegetation and its organic matter increases soil nutrients, our aim was to understand the effect of hurricane disturbance in fungal communities, with special interest in mycorrhizal network. In 2015, Patricia hurricane landfall in Pacific coast, soil and root samples of ectomycorrhizal hosts were taken one and two years after hurricane, then they were sequenced with Illumina MiSeq. Also we obtained environmental data to categorize the disturbance. Litterfall increased soil nutrients one year after hurricane, however we found a decrease in soil fungal communities, same as roots. Fungal communities had a drastic turnover, and we found positive regression of light with rhizospheric fungal diversity, and negative regression with soil temperature. Ascomycota was the most diverse group in each sample. Saprotrophs were the most common fungal guild in the high disturbance sites; arbuscular mycorrhizae were absent in high disturbance plots and common in recovery plots. Even if we found mycorrhizal species, the network was disconnected in 2016, i.e. there were not share species. Two years after hurricane, rhizospheric communities recover opposite to soil community. Fungal communities were not resistant but at medium-term they can be resilient.
Unraveling the endophytic diversity associated with Rubiaceae tropical plants and the ecological factors driving community assemblage.

TUES 16

Humberto Castillo Gonzalez¹, Ana Alonso², Phillip Staniczenko³, Jason Slot⁴, Priscila Chaverri¹,⁵

¹University of Maryland, College Park, USA. ²Biodiscovery Institute, University of North Texas, Denton, USA. ³City University of New York, Brooklyn, USA. ⁴Ohio State University, Columbus, USA. ⁵Center for Natural Products Research (CIPRONA), University of Costa Rica, San José, Costa Rica

Abstract

The ecological drivers of endophytic communities (EC) in forests remain largely underexplored. Several studies have demonstrated that EC composition is influenced by biotic and abiotic factors. For this research, two old growth forests in Costa Rica were sampled. Fungal EC associated with leaves of several species of wild Rubiaceae were analyzed and studied to determine whether they share a ‘core endophytome.’ Library preparation was performed through ITS nrDNA metabarcoding (Ion Torrent) and diversity was assessed using a variety of packages in RStudio (i.e., DADA2, phyloseq, CatchAll). We proposed an ecological network analysis to model the community structure and our study revealed key hub microorganisms. A mixed effect model was used to characterize the effect of several drivers of the endophytome and we could ascertain that Rubiaceae-associated EC are determined by plant species, location and tissue developmental stage. We highlight the importance of the former because colonization frequency and species were higher in mature leaves than in juvenile. A t-test revealed no overall difference in chemoprofile as a function of leaf age; however, there was variation in specific compounds (i.e., 29 out of 224 for Rubioideae subfamily, 22 for Ixoroideae, 1 for Cinchonoideae). This work seeks to assess the biological significance of them. For instance: Are these differential secondary metabolites diffusible to apoplastic fluids or sealed in organelles? Are they fungitoxic? Can fungi evade, tolerate, detoxify, use them? Our findings provide new insights into the mechanisms driving EC assemblage in tropical trees; however, these effects need to be further studied.
Some like it cold: snow algal occurrence and snow chemistry structure fungal communities in alpine snows

TUES 17

Avery Tucker, Shawn Brown
The University of Memphis, Memphis, USA

Abstract

Despite harsh environmental conditions associated with life in late-season alpine snows, such as poor nutrient availability, minimal liquid water availability, and strong solar irradiation, fungi thrive. Previous studies have shown that the snow algae (*Chlamydomonas cf. nivalis*) facilitates heterotrophic communities in alpine snows. Using a community sequencing approach (Illumina MiSeq) incorporating physicochemical data, we investigated how fungal communities are structured by the presence of algal blooms across the United States. Using a tri-paired sampling scheme, we sampled from distinct algal blooms on snow from the center of the algal bloom (maximum algal biomass), the periphery of blooms, and from uncolonized snows adjacent to the bloom. Results indicate a complex network of microbial interactions whereby fungal communities are mainly structured locally by algae and regionally by biogeographical attributes (PERMANOVA). Fungi were also structured by snow oxidation-reduction potential, dissolved oxygen, nitrate levels, pH, resistivity, total dissolved solids, conductivity and salinity, but less extensively based on PERMANOVA analyses. Of the many interesting lineage specific findings, fungi belonging to phylum Chytridiomycota and class Microbotryomycetes show high levels of region specificity where as many fungi were cosmopolitan. Snow communities are dynamic and diverse and are proving to be a reservoir of novel and insofar undescribed fungal biodiversity. Continuing investigations into algae facilitation and nival community development promise to reveal much about snow fungal ecology.
The effect of nutrient addition and herbivore exclusion on fungal endophyte community diversity within *Andropogon gerardii* tissues.

**TUES 18**

*Monica Watson, Kathryn Bushley, Georgiana May*

University of Minnesota, St Paul, USA

**Abstract**

Fungal endophytes, asymptomatic symbionts within plants, are known to affect plant growth in different environmental conditions, but how does environment affect the communities of fungal symbionts within plants? We examined the impacts of nutrient availability and herbivory on endophyte communities in *Andropogon gerardii* to determine if either factor changes the fungal communities within plants and how the combined factors affect those communities. The experimental fields at Cedar Creek Nutrient Network afforded an opportunity to test the effects and interactions of nutrient availability (fertilizer) and herbivore presence (fencing) was modified in plots in a full factorial experiment. *Andropogon gerardii*, big bluestem, and its fungal endophytes served as a model system. Three different tissue types, new leaves, mature leaves, and stems, were collected to determine if there are different endophyte communities within the plant host and if those communities were affected differently by experimental treatment. Collected tissue was surface sterilized, sectioned, and cultured. Emerging fungi were sequenced at the ITS region for identity and community analyses are being performed to characterize community composition and determine how communities are affected by the different treatments. I expect decreased fungal community diversity in plants grown in nutrient treated plots, and increased diversity in plots with herbivore exclusion. Understanding how herbivory and nutrient addition interact to affect the fungal communities within plants is critical to practical land management decisions and agricultural applications.
Comparison of long and short amplicon metabarcoding to determination of fungal species diversity and spatial turnover in an ectomycorrhizal West African woodland

TUES 19

Brendan Furneaux¹, Mohammad Bahram², Nourou Yorou³, Anna Rosling¹, Martin Ryberg¹

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Abstract

Long-read high-throughput sequencing promises to increase taxonomic coverage of environmental barcoding studies through decreased sequencing length bias and the opportunity to use highly conserved primers, while also improving the ability to place novel sequences taxonomically. However, these advantages come at a significantly higher cost per base pair read, and amplification of long regions may increase PCR length bias and the formation of artifacts such as chimeras. We compare the results of two different primer pairs in an actual ecological study to determine whether the choice of amplicon length can lead to substantially different conclusions.

We collected soil samples from two 25m transects with 1m sample spacing in *Isoberlinia doka* dominated ectomycorrhizal woodlands in Benin in two consecutive years. Extracted DNA was amplified with two different primer pairs targeting ribosomal DNA regions: gITS7-ITS4, targeting the ITS2 region, and ITS1-LR5, targeting the full ITS region as well as approximately 900 bp of LSU, and then sequenced using PacBio SMRT technology. We compared the diversity recovered by each method, as well as the ease of assigning taxonomic classifications. Finally, we compared the spatial community turnover rate as assessed by both species-based and phylogenetic community dissimilarities.
Life in the leaves: diversity and distribution in foliar fungal endophytes

TUES 20

Austen Apigo¹, Rodolfo Salas-Lizana², Jose Rubén Montés², Edward Allen Herre³, Luis Mejía⁴, Ryoko Oono¹

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Abstract

Foliar fungal endophytes (abbreviated as ‘endophytes’) are a species-rich and phylogenetically diverse guild of microfungi that asymptotically inhabit the aboveground, tissues of all land plants. Endophytes are distributed across every terrestrial biome and it has been suggested they compose much of the undiscovered biodiversity within the kingdom Fungi. However, their apparent ‘hyperdiversity’ has yet to be quantified (1) across the diversity of ecosystems in which they occur, (2) with culture-independent methods that capture rare and unculturable fungal species and (3) with analyses that account for host community structure. To understand how the structure of these complex symbioses vary with climate and the plant host community, we surveyed endophyte communities from 21 temperate and tropical forests (5°N - 64°N) by intensively sampling all co-occurring plant host species within five 50 m² quadrats per site during the summers of 2016 and 2017. We then sequenced the ITS1 region on the Illumina MiSeq platform to directly characterize fungal community structure from host leaf tissue (n = 2,424 plant samples). Previous culture-dependent studies suggest endophytes are highly abundant and diverse in the tropics and follow the widely documented pattern in many plants and animals where species richness increases towards the equator - the latitudinal diversity gradient. Our preliminary high-throughput data (12 of 21 sites) suggest endophyte diversity is bimodal as a function of latitude. I will discuss how plant community structure and host specificity may contribute to observed endophyte diversity patterns and the implications of endophyte diversity on our understanding of global fungal biodiversity.
A novel *Fusarium* induces putative pseudoflowers on yellow-eyed grass (*Xyris* spp.) in Guyana

**TUES 21**

Imane Laraba¹, Hye-Seon Kim¹, Martha Vaughan¹, Mark Busman¹, Robert Proctor¹, Susan McCormick¹, Kerry O’Donnell¹, Catherine Aime², Rachel Koch², Kenneth Wurdack³

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**Abstract**

We discovered a novel *Fusarium* species that produces putative pseudoflowers on three perennial species of *Xyris* (yellow-eyed grass) in Guyana. A rosette of ultraviolet reflective petaloid structures that mimic host flowers in color, shape and size were produced on infected plants. This is the first report of a *Fusarium* producing pseudoflowers. Multilocus molecular phylogenetic analyses of data mined from whole genome sequences resolved the novel *Fusarium* pathogen as sister to *F. pseudocircinatum* within the African clade of the *F. fujikuroi* species complex. The *Xyris* pathogen is phenotypically distinct from all other *Fusarium* species in that it produces abundant erect 0-septate microconidia-bearing synnemata up to 2 mm in height on carnation leaves. The potential of this pathogen to produce biologically active compounds, including phytohormones, pigments and mycotoxins, was assessed by conducting BLASTn searches of whole genome sequence data. Mycotoxin production was also assessed by liquid chromatography–mass spectrometry (LC-MS) analyses of strains cultivated in vitro on a solid medium. Results of a PCR assay for mating type revealed that MAT1-1 and MAT1-2 idiomorphs were both present on the flower-like rosettes on *X. surinamensis* and *X. setigera*; however, single conidial isolates only possessed one of the idiomorphs. We speculate that this putatively heterothallic fungus is deceiving unknown plant pollinators into vectoring microconidia of mating compatible strains to the same host plant. SEM images and results of a species-specific PCR assay revealed that the fungus had established a systemic infection in the sterilized plants that were producing floral mimics.
Molecular phylogeny reveals novel evolutionary lineages of *Curvularia* from Sri Lanka

**TUES 22**

Himashi S. Ferdinandez, Dhanushka Udayanga, Nelum Deshappriya, Mayuri Munasinghe, Dimuthu Manamgoda

University of Sri Jayewardenepura, Nugegoda, Sri Lanka

**Abstract**

The genus *Curvularia* comprises phytopathogenic fungi causing diseases on cereals and grasses. The species of *Curvularia* can be also found as endophytes or saprobes on dead material of plant hosts and are known to be opportunistic human pathogens on immunocompromised patients. The *Curvularia* species that cause diseases on staple crops, wild relatives and weeds in Sri Lanka are poorly known. Insufficient data on identifications of emerging fungal diseases can be a threat on both commercial cultivations as well as small scale farmlands. Therefore an assessment of *Curvularia* species associated with cereal crops, their relatives and weeds is vital, regarding crop and fiber security of the country. The major objective of this study was to collect *Curvularia* spp. from cereal crops, their wild relatives and weeds in Sri Lanka, to accurately identify them and to establish their evolutionary relationships. Fresh collections of about 20 isolates of *Curvularia* were used in this study collected from thirteen different locations across four provinces. Fungi were isolated and morphological characters were assessed based on digital imaging. Molecular phylogenetic analyses were performed for the fresh collections from this study along with available ex-type species for ITS and GPDH loci. The combined analysis revealed that the common occurrence of *C. affinis, C. geniculata* and *C. dactyloctenicola* from different hosts. At least five species were distinct from known species based on current phylogeny and considered to be potentially novel lineages within the genus. Therefore, the results suggest an unexpected diversity within limited geographic region of the Island.
Anchored Hybrid Enrichment For Selective Genome-Level Phylogenetic Analysis of Fungaria Samples: The *Tuber rufum* clade as a case study

Arthur Grupe¹, Alija Mujic², Michelle Jusino¹, Rosanne Healy¹, Scott McCoy², Gregory Bonito³, Zoltán Bratek⁴, lilla Bóna⁵, Akihiko Kinoshita⁵, Li Fan⁶, Vasileios Kaounas⁷, Gonzalo Guevera⁸, James Trappe⁹, Matthew Smith¹

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Abstract

Anchored hybrid enrichment, or “target capture” is a tool that uses genomic sequence data to mine exons and their flanking intronic regions, called “splash zones”. This method uses custom RNA “baits” that bind to exons of putative single copy protein-coding genes that are selected to improved phylogenetic inferences. Target capture facilitates sequencing of selected phylogenomic markers from large numbers of samples that might otherwise be too costly for whole-genome shotgun sequencing due to large genome sizes, or because of degraded DNA from museum fruiting bodies. Target capture has been used in phylogenomic studies of plants and insects from museum collections but has never been applied to fungal collections. To test the application of target capture on fungal herbarium samples, we initiated a study of the *Tuber rufum* clade, which includes numerous cryptic species that are poorly resolved with traditional molecular markers. Genomes within Tuberaceae range from ~90–192+ million base pairs, therefore sufficient sequencing without selection of markers would be prohibitively expensive. Ninety-six specimens ranging in age from 2–114 years and representing phylodiversity across the clade were sampled from 14 fungaria. Custom baits were designed based on four Tuberaceae genomes. After filtering, 1,437 proteins produced 43,844 candidate baits with 2X tiling that were then parsed to the 20,020 limit of the selected kit. We will discuss the phylogenomic results, the methods and modifications we employed, and will discuss the prospects of future use of this approach in future mycological research.
Unwrapping the mummy: solving the phylogenetic mystery of the arthropod-mummifying fungus

TUES 24

Kevin Amses¹, Matthew Smith², Timothy James³

¹University of Michigan, Ann Arbor, USA. ²University of Florida, Gainesville, USA

Abstract

The genus *Neozygites* is composed of twenty-three species of entomopathogenic fungi that infect and kill aphids or mites with a high degree of specificity. Under specific, transient environmental conditions, species of *Neozygites* can facilitate epizootic infections – widespread but temporary mass killings of hosts in an area. After succumbing to the infection, host cadavers become mummified and house the parasite's resting stage until favorable infection conditions return. *Neozygites* occupies an ambiguous seat in the Entomophthorales (Zygomycota s.l.) based on morphology that is largely unsubstantiated by molecular markers. This part of the tree has recently undergone substantial reorganization in lieu of genome-scale phylogenetic data. The complications involved in culturing *Neozygites* under laboratory conditions coupled with abnormal and poorly aligning rDNA sequences have long obscured its position in multigene phylogenies, and whole genome data has never been available. A classic case of long-branch attraction in comprehensive phylogenies of the kingdom, the phylogenetic placement of *Neozygites* remains obscured. We have employed a single-cell genomic approach to generate whole genome assemblies for this early-diverging entomopathogen and stand ready to address this long-standing ambiguity in the fungal tree of life.
Surveys of the Everglades reveal new species to the mycoflora of the United States

TUES 25

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Abstract

The Everglades National Park is part of the Caribbean biodiversity hotspot. Despite the unique flora and fauna of the park, little has been done to document the macrofungi of the Everglades, with collections from south Florida peaking in the 1940s. Because of the lack of modern collections from this region, we documented the macrofungi from Everglades National Park from 2018-2019. Voucher specimens, temporarily on loan at the University of South Florida Herbarium, were analyzed using the Internal Transcribed Spacer region (ITS), the fungal DNA barcode. Our results reveal many species of macrofungi for the first time in the United States, including cup fungi, boletoid, and agaricoid species. *Fistulinella gloeocarpa*, a bolete originally described from the West Indies, was found in isolated hammocks. A species of *Gymnopus* originally described from Brazil was found abundantly fruiting in hammocks in the park. *Geodina*, previously only known from Central America and the West Indies, was documented. Our surveys also expanded the southern range of an undescribed bolete. Several other species remain unidentified to the species level and appear to be new finds for Florida.
Taxonomic diversity of the genus *Amanita* in Pakistan

**Amanita**

**TUES 26**

Munazza Kiran¹, Donald H. Pfister², Abdul Nasir Khalid¹

¹University of the Punjab, Lahore, Pakistan. ²Harvard University, Cambridge, USA

**Abstract**

The genus *Amanita* comprises 95% of the species in family Amanitaceae. It has been the focus of interest for various mycologists since its establishment. Species included in the genus are edible as well as deadly poisonous. A large majority of the species are reported to be ectomycorrhizal, thus playing vital role in forest ecology. Pakistan has a great variety of landscapes with diverse topography and thus a high diversity of ecosystems and habitats. The Himalaya, Hindukush and Karakoram mountain ranges host important forests in Pakistan. These have a great and varied fungus associated with the mycorrhizal tree species i.e., *Abies pindrow, Cedrus deodara, Juniperus macropoda, Pinus gerardiana, Picea smithiana, Pinus wallichiana*. In contrast to the global knowledge of the genus, very little is known about this genus in Pakistan. Various fungal forays, over recent years, have indicated that this is an under-sampled geographic region. Our collections and molecular phylogenetic studies have demonstrated that the *Amanita* species from Pakistan can contribute to knowledge of the diversity of this large and important genus. To date 19 species have been recognized and, our phylogenetic studies indicate that there are more to be described.
Coffee berry disease (CBD), a rot of coffee fruits, is a severe but overlooked problem. The known pathogens are several species of *Colletotrichum*, reported from Africa. CBD is common in Puerto Rico. We asked which fungi are the causal agents, and if the coffee berry borer (CBB) is a vector of the pathogens. Fungi were isolated from fruits with CBD, with and without CBB damage. Fungi were identified by morphology and sequences of barcoding genes (ITS, β-tubulin, EF-1α and others). Pathogenicity was tested by inoculation on artificially-wounded coffee fruits. Fruits were also placed in bags with CBBs inoculated with potential pathogens to test if the fungi were pathogenic and the CBB was a vector. Inoculated fruits were inspected for signs of CBD. Several species of *Colletotrichum* and *Fusarium* were isolated and some were shown to be pathogens using Koch's postulates. Some of these species were also isolated from coffee berry borers, showing that the CBB can be a vector. These results expand the range of fungi known to cause CBD. They provide additional incentive to control CBB infestation because the CBB can be a vector of coffee fruit rot pathogens.
Fungal-Bacterial Networks Structuring Biocrust in Mojave Desert, USA

TUES 29

Nuttapon Pombubpa¹, Nicole Pietrasiak², Paul De Ley³, Jason E. Stajich¹

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Abstract

Biocrusts are recognized as the living skin of drylands containing diverse microorganisms that are essential to desert ecosystems. However, research largely focused on surface external morphology without examining microbial communities. Moreover, when biocrusts’ microbial composition has been examined, bacteria are typically the only target community. Thus, our project aims to explore the composition of both fungi and bacteria, to investigate characteristics structuring biocrust microbial identity, and to evaluate biocrust fungal-bacterial networks amongst a set of biocrust community types. We used Illumina Miseq amplicon sequencing to assess composition and structure of bacterial and fungal communities. Biocrusts surface and subsurface soils were collected from Joshua Tree National Park (JTNP), Granite Mountain (GMT), Kelso Dunes (KELSO) and Cima volcanic location (CIMA) within Mojave Desert, USA. Five biocrust types were examined: Light-algal crust (LAC), Cyano-lichen crust (CLC, Collema sp.), Green-algal lichen crust (GLC, Clavacidium sp.), Smooth moss crust (SMC, Bryum sp.), and Rough moss crust (RMC, Syntrichia sp.). We found that main characteristics structuring biocrust were 1) geographical patterns which differentiate central Mojave sites (GMT, KELSO, CIMA) from JTNP and 2) soil depth patterns which differentiate surface from subsurface microbial communities. Bacterial-fungal network analysis revealed LAC networks were similar between surface and subsurface, while lichen crusts (GLC and CLC) contained less networks on surface, and moss crusts (SMC and RMC) had more networks on surface. In summary, we found key patterns structuring microbial communities. Recognizing these patterns and how they affect biotic networks, and potential functions provide crucial information for biocrusts restoration and management.
Freshwater fungal diversity and ecological interactions with mosquitoes and plant communities

TUES 30

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Abstract

Aquatic fungi perform important and complex functions in freshwater ecosystems including the degradation of plant litter and nutrient cycling. However, other ecological roles of freshwater fungi remain to be determined. The purpose of this project is to describe fungal communities in an urban stream and examine potential endophytic links between riparian tree fungi and aquatic fungal communities and its interactions with mosquitoes. Fungi were baited using apples, pears, and cherries in an urban stream in west central Illinois from April through November 2016. To test the hypothesis that aquatic yeasts may have a potential endophytic niche as part of their life cycle, leaves were collected from tree species at sites where fungal traps were placed. Leaf punches were surface sterilized and plated on two types of media (EYSA, YG) and incubated at 25°C and 6°C. All fungal isolates from the traps and leaves were identified using ITS rRNA gene sequencing, resulting in 53% of all fungi cultures identified as yeasts with 40% of the OTUs closely related to endophytes or insect associated fungi. The most abundant genera cultured from the urban stream were Meyerozyma, Candida, Pichia, and Cryptococcus. Leaves also contained Meyerozyma and Rhodotorula. These yeasts are associated with mosquito microbiota. Bioassays were conducted to determine the effect of yeasts on mosquito egg hatching indicated interactions from mutualistic (Cryptococcus, 89%) to antagonistic (Pichia, 8%). Mosquitoes are widely distributed and are important vectors for many human pathogens. However, the nature of the interactions between mosquitoes and fungi remains mostly unknown.
Elucidating the phoretic fungal community of root-feeding beetles in the Georgia Piedmont

TUES 31

Megan Buland¹, Brittany F. Barnes¹, Kier D. Klepzig², Kamal J.K. Gandhi¹, Caterina Villari¹

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Abstract

In recent decades, Grosmannia species (of the blue-stain fungal group) and their root-feeding beetle vectors (Hylastes, Hylobius and Pachylobius spp) have been associated with areas of loblolly pine mortality in the Piedmont region of Georgia, however their potential role in host mortality is unestablished. Study objectives are to: 1) determine the phenology of loblolly pine associated root-feeding beetles in Georgia, 2) assess the blue-stain fungi community associated with these beetles and whether this association varies in stands with differing management practices and across seasons.

Root-feeding beetles were live trapped in two loblolly pine stands with differing management histories (prescribed burned within the last 1-2 years vs unburned), from May 2017 - October 2018. Across vectors, abundance varied over time, peak catches within a species occurred at similar times in both stands. Preliminary identification of vector derived pure cultures included G. profanum, G. huntii and G. alacris. While the latter two have been previously associated with loblolly pine, G. profanum is unexpected, as the fungus was thought to only occur on hardwoods, and not believed to be beetle vectored. To elucidate the blue-stain fungal community associated with each vector species, a subset of each beetle vector has been analyzed with a metabarcoding approach, using the β-tubulin gene as a target region. Metabarcoding facilitates identification of the whole fungal community, including species potentially overlooked using traditional isolation methods, and enables quantitative comparison of fungi between vectors. Results of this study will lay the groundwork for future understanding of this system in the Piedmont.
Developing a mycoinsecticide for *Dendroctonus rufipennis*: Phenotypic and experimental differences in *Beauveria bassiana* isolates from the Rocky Mountain region

TUES 32

Andrew Mann, Seth Davis
Colorado State University, Fort Collins, USA

Abstract

The ubiquitous insect-killing fungus *Beauveria bassiana* is widely used as a biological control agent to treat a variety of arthropods ranging from mites to beetles. *Dendroctonus rufipennis* has been responsible for the death of 17 million *Picea engelmannii* trees over the past two decades and is currently considered to be one of the major forest pests in western North America. Despite the promise that *B. bassiana* brings as a form of augmentative biological control against *D. rufipennis*, a recent laboratory evaluation did not lead to successful field application likely due to a lack of cohesion between environmental conditions that *D. rufipennis* and *B. bassiana* prefer. We tested 14 *B. bassiana* isolates from the Rocky Mountain region for their growth and pathogenicity in a series of environmental assays representative of the *D. rufipennis* study system such as a range of temperatures, competition with the spruce beetle symbiotic fungus *Leptographium abietinum*, constitutive and induced concentrations of five *Picea engelmannii* monoterpenes, varying levels of water potential, a nutrient limited environment, and sunlight. We demonstrate that (1) genotypically similar *B. bassiana* isolates vary widely in their growth response to environmental conditions, even when isolated from similar habitats and sources; (2) tree phytochemicals are highly inhibitory to *B. bassiana* growth, especially at induced concentrations, though low temperatures also strongly reduce growth; (3) the interpretation of isolate virulence can differ substantially depending on assay and experimental design. These collective findings have implications for the field application of *B. bassiana* as a bark beetle control agent.
Soybean (Glycine max) hosts nematicidal fungal community in soybean cyst nematode-infested fields

TUES 33

Noah Strom¹, Weiming Hu², Deepak Haarith¹, Senyu Chen³, Kathryn Bushley¹

¹University of Minnesota, Saint Paul, USA. ²University of Florida, Gainesville, USA. ³University of Minnesota, Waseca, USA

Abstract

Fungal endophytes can provide protection to plants from insect herbivores and microbial pathogens. The soybean cyst nematode (SCN, Heterodera glycines), a root-feeding pathogen of soybean (Glycine max), is commonly managed through rotation of soybeans with corn (Zea mays), a non-host of the SCN. However, few studies have examined root endophytic communities of these crops for fungi with SCN-antagonistic activity. The objective of our study was to test whether culture filtrates produced by soybean and corn root endophytes can kill the SCN. A total of 626 fungal endophytes were isolated from surface-sterilized roots from experimental plots in which soybeans and corn had been grown under annual rotation and under 1, 3, 5, and 35 years of continuous monoculture. Fungal isolates were grouped into 401 morphotypes, which were clustered into 108 operational taxonomic units (OTUs) based on 99% sequence similarity of the full ITS region. A minimum of 10% of morphotype representatives within each OTU were grown in malt extract broth (MEB) and in a secondary metabolite-inducing medium buffered with ammonium tartrate (SMAT), and their culture filtrates were tested for nematicidal activity against SCN juveniles. Nematicidal activity of isolates belonging to the same OTU was variable, but several OTUs assigned to the genus Fusarium consistently contained nematicidal members. Other nematicidal isolates included members of the genera Epicoccum, Exophiala, Hirsutella, Myrothecium, and Trichoderma. Mean nematicidal activity was greater in soybean plots with higher SCN density, suggesting that pathogen pressure promotes the development of an SCN-antagonistic root endophytic community.
High throughput ITS identification of Culturable Soybean Cyst Nematode Cyst Mycobiome: A *Fusarium* Story

TUES 34

Deepak Haarith¹, Weiming Hu², Dong-gyu Kim³, Senyu Chen¹, Kathryn Bushley¹

¹University of Minnesota, Saint Paul, USA. ²University of Florida, Gainseville, USA. ³University of Minnesota, Minneapolis, USA

Abstract

Soybean Cyst Nematodes (SCN) are the most economically devastating pathogen on soybean worldwide. Current management methods such as crop rotation may be economically unsustainable and genetic resistance for this pathogen is already being overcome by races of the SCN. Chemical nematicides like methyl bromide are banned for their deleterious effects on human health and the environment. Biological control is an attractive alternative option, but there are no commercially available fungal biocontrol agents for SCN. Thus, it is important to characterize the SCN cyst mycobiome to better understand fungi inhabiting this environment and identify potential biocontrol agents. Fungi were isolated from 6000 SCN cysts collected over six sampling times across three years from a long-term soybean-corn rotation experiment in Waseca, MN. These experimental plots consisted of several soybean-corn rotations including annual and five-year rotation and continuous monoculture. The fungi obtained were grouped into 1654 morphogroups based on their colony morphology on PDA, and the ITS region was sequenced for one representative isolate from each morphogroup (morphotype). All morphotypes were identified to genus based on BLAST search to both the NCBI and UNITE databases. Morphotypes were then clustered based on 99% or higher similarity of the ITS sequence using the UClust algorithm. *Fusarium* was the most frequently isolated genera and contributes to about 40% of all fungi isolated from this study. To study the diversity of this major group, multi-locus sequence analysis was performed on a representative of each of the 28 *Fusarium* clusters using EF1a, RBP2, 28s RNA, and b-tubulin genes.
Cinnamic acid as an inhibitor of growth, flavonoids exudation and endophytic fungus colonization in maize root

TUES 35

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Abstract

Cinnamic acid (CA) is an allelochemical that inhibits the growth of root promoting soil microorganisms. To prevent the growth of soil microbes, CA modulates several metabolic pathways in host plants and soil microbes. The aim of the current study was to investigate the effect of CA on maize root growth, exudation of secondary metabolites and its interaction with beneficial endophyte Pz11. The endophyte Pz11 was isolated from the roots of drought stressed Asphodelus tenuifolius (wild onion). The F. culmorum Pz11 produced phytostimulants and signaling compounds, such as indole-3-acetic acid (IAA), flavonoids and sugars. Moreover, the strain have effectively colonized the roots of maize and subsequently enhanced the growth of its host plants. On the contrary, application of CA has reduced root growth in maize seedlings as well as root colonization ability of P. culmorum Pz11. Also, maize seedlings exposed to CA exude low quantities of flavonoids and polyphenols. In conclusion, CA reduces the maize root growth and exudation of secondary metabolites, which may affects its ability to attract plant growth promoting endophytic fungi.
Cell plasticity and disease manifestation in *Cryptococcus*

**TUES 37**

Kenya Fernandes⁠¹, Adam Brockway⁠², Miriam Haverkamp⁠³, Christina Cuomo⁠⁴, Floris van Ogtrop⁠², John Perfect⁠⁵, Dee Carter⁠²,⁶

¹University of Sydney, Darlington, Australia. ²University of Sydney, Sydney, Australia. ³Faculty of Medicine, University of Botswana, Botswana. ⁴Broad Institute, Boston, USA. ⁵Duke University, Durham, USA. ⁶Marie Bashir Institute, Sydney, Australia

**Abstract**

*Cryptococcus*, normally described as a spherical encapsulated yeast of ~7 µm diameter, can display considerable heterogeneity in size and shape. Giant cells >15 µm, micro cells <2 µm, irregularly shaped cells, and cells with enlarged or shed capsule have been described *in vivo* and *in vitro*, however their association with virulence and disease progression is not well understood. In this study we obtained isolates of *C. neoformans* and *C. tetragattii* from HIV-AIDS patients in Botswana along with detailed clinical data. Using conditions designed to simulate host infection we assessed each strain for the presence of cell morphotypes and correlated their presence with cellular and clinical parameters. Giant cells were on a spectrum of increasingly larger cells, while micro cells appeared to be an independent cell type and were associated with extracellular capsule. The presence of larger cells and capsules was positively correlated with higher CD4+ T-cell count and negatively correlated with indicators of intracranial pressure, while micro cells and shed capsule had opposite associations and were negatively associated with indicators of cerebral inflammation. This suggests that larger cell types are more likely to occur in early stage infection when CD4 count is still high and intracranial pressure is relatively low, and this transitions to smaller cell phenotypes with disease progression, when micro cells and shed capsule may also act to dampen the host immune response. These data suggest that cell plasticity is important for virulence, can alter over the course of infection and is likely to be epigenetically determined.
Interaction and rupture of *Candida albicans* on Nanostructured surface of Cicada wing.

**TUES 38**

*Naga Venkatesh Kollu, Dr. Dennis LaJeunesse*

University of North Carolina at Greensboro, Greensboro, USA

**Abstract**

Microorganisms attach to surfaces and produce extracellular polysaccharides, resulting in the formation of biofilm which poses a serious problem for public health because of the increased resistance of biofilm-associated organisms to antimicrobial agents and infections in patients with indwelling medical devices. Candidiasis is usually associated with these indwelling medical devices. Studies have shown that nanostructured surfaces (NSS) found on insect wing and cuticles, rupture and kill adhered microbes, the nanoscale topography is directly responsible for this effect. The goals of this research are to characterize the nanoscale mechanical interactions between a pathogenic yeast cell, Candida albicans and cell-rupturing NSS and to define the conditions that determine and control NSS-induced *C. albicans* cell rupture. We define the mechanical roles of the yeast cell wall in the evolution of fungal-host interactions, especially in the context of drug-resistance. The initial adhesion and rupture of Candida spp. on NSS versus time was studied using confocal laser microscopy and confirmed using Scanning electron microscopy. The mechanical modulus required for the rupture of Yeast cell will be calculated using an atomic force microscope in comparison to the nanostructured surface which might lead to the manufacture of advanced synthetic-NSS coating for indwelling medical devices. We determine how resistance to current antifungal drugs physically change *C. albicans* cell which alters the mechanical properties of that cell and its interactions with NSS. The long-term goals are to use this information to design and apply NSS as a mechanical means of controlling pathogenic fungal growth and biofilm formation.
Further Ultrastructural Studies on the Spore Bodies of Orbiliomycetes

TUES 39

James Mitchell\textsuperscript{1,2}, Rosanne Healy\textsuperscript{3}, Luis Quijada\textsuperscript{1,4}, Richard Schalek\textsuperscript{5}, Jeff Lichtman\textsuperscript{5,6}, Donald Pfister\textsuperscript{1,4}

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Abstract

Ascospores of the fungi in Orbiliomycetes are characterized by the presence of one or more "spore bodies." These mysterious subcellular structures, located at the apices of the spores in most taxa, come in many different shapes and sizes depending on the taxa involved. Their appearance is, in fact, often an important taxonomic feature, which to a certain extent is supported by molecular data. They are refractive, and sufficiently small that traditional light microscopy reveals little about them other than their presence and shape. As a result, not much is known about their ultrastructure, composition, function, or development. Although not all of these open questions can be addressed with any single technique, electron microscopy is well suited to address questions regarding structure and development. Some transmission electron microscopical (TEM) work has been done on these spore bodies in the past (Benny, Samuelson & Kimbrough 1978; Kumar et al. 2011; Healy & Pfister unpublished), with inconclusive or unconvincing results. The current work builds on past efforts by applying a different technology, the ATUM (automated tape-collecting ultramicrotome), and instead performing serial section scanning electron microscopy (ssSEM), a combination of tools normally used in neuroscience. This has allowed, for the first time, the generation of three-dimensional image stacks at high resolution of entire spore bodies, both developing and mature, allowing us to more accurately address questions of their origin and structure.
Ontogeny of the endocytic collar in filamentous fungi

TUES 40

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Abstract

Hyphal morphogenesis depends mainly on the establishment and maintenance of polarized growth. This is accomplished by the orderly migration and discharge of exocytic vesicles carrying cell membrane and wall components. We have been searching for evidence that endocytosis, an opposite process, could also play a role in hyphal growth and conidial germination. We analyzed proteins involved in the different stages of endocytic vesicles formation (AP180, SLA1, LAS17, MYO-1, ARP2/3, FIM-1, CRN-1) and their respective deletion mutants during the various stages of development in the filamentous fungus Neurospora crassa. We found that patches labeled with endocytic reporters accumulate in the apex of the germinating tube of conidia. This position is maintained until the germ tube reaches about 150 microns thereafter patches begin to form a collar in the subapex, a conspicuous localization maintained in mature hyphae.
Surveying the NPFxD motif-containing proteins in *Aspergillus nidulans*

TUES 41

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Abstract

Filamentous fungi produce polarized cells called hyphae by synthesizing and adding new membrane and cell wall exclusively at the apex. Polarized hyphal extension is maintained by an apical recycling mechanism that balances endocytosis and exocytosis at the forefront of growth. This equilibrium requires an apical formation of secretory vesicles deemed the Spitzenkörper (SPK), as well as an endocytic sub-apical collar located approximately 1-5µm distal to the SPK, where cargoes are internalized. Evidence of this relationship is observed through the investigation of landmark proteins along the plasma membrane that mark areas of impending growth. In *Aspergillus nidulans*, 39 proteins are each predicted to be cargo of endocytosis based on the presence of an NPFxD motif, which is a necessary endocytic signal sequence in yeast, and those that are cargoes for endocytosis are also likely to be associated with the establishment or maintenance of polarized growth. I hypothesize that NPFxD motif-containing proteins that are cargoes for endocytosis will localize to at least one of three apical regions (the SPK, sub-apical collar, and apical dome) where cargoes are typically observed. To test this, the expression and dynamic localization of motif-containing proteins is evaluated by endogenously inserting GFP. The localization patterns studied thus far support the hypothesis, as do the deletion phenotypes. Mutants display atypical development in various cell types and an inability to maintain polarization, which further suggests that the genes in question are involved with membrane turnover. Cell shape, FM4-64 uptake, and sexual reproduction was also evaluated in each deletion strain.
Reverse fountain streaming: An analysis of hyphal cytoplasmic flow in the zygomycetes

TUES 42

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Abstract

The zygomycetes comprise a diverse group of filamentous, non-flagellated fungi, whose emergence has been correlated to the transition from an aquatic to terrestrial habitation. During hyphal tip elongation, the function and behavior of the apical vesicle crescent (AVC) and the Spitzenkörper (Spk) have been important areas of research. Fewer studies, however, have examined patterns of cytoplasmic flow in growing hyphae. Fungi in the Dikarya, such as Neurospora crassa, exhibit unidirectional anterograde cytoplasmic flow, i.e., sleeve-like streaming. We will present several examples where growing hyphae of zygomycetes exhibit a bi-directional pattern of cytoplasmic flow. This pattern is characterized by an anterograde streaming along the cortical subapical hyphal region followed by a change in the apical dome to a retrograde streaming down the central axis of the cell. While this mode of cytoplasmic flow, known as reverse fountain streaming, is common in some tip-growing plant cells, e.g., pollen tubes and root hairs, to date this behavior has not been reported in fungal hyphae. Results will relate the dynamics of cytoplasmic flow with hyphal diameter, rates of growth, and the presence of an AVC or Spk in zygomycete hyphae. Implications of these results will be discussed in regard to biology of hyphal growth and zygomycete evolution.
Microfluidic Studies of Fungal Growth Rate and Pattern

TUES 43

Michelle Momany\textsuperscript{1}, Alex Mela\textsuperscript{1}, Alex Hopke\textsuperscript{2}, Felix Ellett\textsuperscript{2}, Daniel Irimia\textsuperscript{2}

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Abstract

Fungi thrive in a variety of environments where they overcome many obstacles in the search for food and mates. Those obstacles include competing microorganisms and physical barriers. Though much work has been done examining growth rates and patterns of individual fungi, few studies have directly compared these factors among different species. We designed microfluidic devices to allow the observation of fungal growth rate and response to microscale obstacles. Fourteen fungal strains representing eight species were recorded in microfluidic devices through the crowdsourced project “The Fungus Olympics.” We found that maximum growth rates among the fungi participating in the study varied between 1 and 6 microns/minute. The ability of fungi to navigate microscale mazes varied depending on the maze design, with some mazes favoring faster growth speed and some favoring more frequent branching. Future Fungus Olympics competitions will expand the number of filamentous fungi tested and probe further the apparently inverse relationship between speed and branching.
Probing the mechanistic basis of behavior manipulation using the "zombie" entomopathogen *Entomophthora muscae*.

**WED 1**

Carolyn Elya, Benjamin de Bivort
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**Abstract**

Many microbes induce striking behavioral changes in their animal hosts, but the underlying molecular mechanisms are poorly understood. This is due in part to the difficulty of studying non-model organisms with limited tools. I discovered a strain of the fungal behavior-manipulating fly pathogen *Entomophthora muscae* infecting wild drosophilids and developed methods to propagate the fungus in lab-reared *Drosophila melanogaster*. Before sunset on their final day of life, my infected flies manifest the moribund behaviors characteristic of *E. muscae* infections: they climb to a high location, extend their proboscises, and raise their wings in a pose that is ideal for spore dispersal. In characterizing the course of infection, I discovered that *E. muscae* invades the host nervous system, which could provide a direct route for altering host behavior. I am now focusing on understanding the mechanism underlying sumitting behavior, hypothesizing that the fly’s endogenous gravitactic circuitry is manipulated by the fungus to induce upward climbing immediately before death. I have developed a high-throughput assay to measure sumitting behavior and found that flies consistently undergo a burst of activity immediately preceding death. This newly-uncovered activity element of sumitting behavior suggests that the fungus may be inducing an internal arousal state in addition to or instead of manipulating gravitactic circuitry to position the fly for optimal fungal dispersal. I next aim to identify the neurons needed for fungal-induced sumitting by performing a neuronal inactivation screen and to perform biochemical analysis of hemolymph from sumitting animals to identify fungal molecules that elicit sumitting behavior.
Genomic Signatures of Nematode Parasitism

WED 2

Kathryn Bushley¹, Thomas Kim², Deepak Haarith², Kathryn Bushley²

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Abstract

Fungal pathogens and parasites of nematodes are scattered across diverse lineages of the fungal tree of life and are capable of infecting diverse species and life-stages of their hosts. Yet, the mechanisms of parasitism and how nematode parasites differ from closely related taxa with differing ecological lifestyles has not been fully characterized. Previous studies have implicated several families of secreted enzymes, including carboxypeptidases, subtilisins, and carbohydrate active enzymes, particularly chitinases, in the infection process. Others, such as secondary metabolite toxins, have been less well investigated. Using comparative genomic and transcriptomic approaches, we identify gene families with potential roles in virulence and address the extent to which these are shared across different lineages of nematode pathogens. In order to characterize mechanisms of parasitism of distinct guilds of nematode pathogens, we compare transcriptomic responses of a nematode trapping fungus (Arthrobotrys sp.), an egg-parasite (Pochonia sp.), and an endoparasite (Hirsutella sp.) to identify arsenals of enzymes and secondary metabolite clusters specialized for these different modes of nematode parasitism.
Drugs, bugs, and fungal plugs: psychoactive plant- and mushroom-associated alkaloids from two behavior modifying cicada pathogens

**WED 3**

Matthew Kasson¹, Emile Gluck-Thaler², Jason Slot², Jason Stajich³, William Davis⁴, Tim James⁴, John Cooley⁵, Daniel Panaccione¹, Jorgen Ellenberg⁶, Henrik De Fine Licht⁶, Angie Macias¹, Matthew Berger¹, Kristen Wickert¹, Cameron Stauder¹, Ellie Spahr¹, Matthew Maust¹, Amy Metheny¹, Chris Simon⁵, Gene Kritsky⁷, Kathie Hodge⁸, Richard Humber⁹, Terry Gullion¹, Dylan Short¹⁰, Teiya Kijimoto¹, Dan Mozgai¹¹, Nidia Arguedas Nidia Arguedas¹², Matt Kasson ¹

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**Abstract**

Entomopathogenic fungi routinely kill their hosts before releasing infectious spores, but select species keep insects alive while sporulating, which enhances dispersal. Transcriptomics and metabolomics studies of entomopathogens with post-mortem dissemination from their parasitized hosts have unraveled infection processes and host responses, yet mechanisms underlying active spore transmission by Entomophthoralean fungi in living insects remain elusive. Here we report the discovery, through metabolomics, of the plant-associated amphetamine, cathinone, in four *Massospora cicadina*-infected periodic cicada populations, and the mushroom-associated tryptamine, psilocybin, in annual cicadas infected with *Massospora platypediae* or *Massospora levispora*, which appear to represent a single fungal species. The absence of some fungal enzymes necessary for cathinone and psilocybin biosynthesis along with the inability to detect intermediate metabolites or gene orthologs are consistent with possibly novel biosynthesis pathways in *Massospora*. The neurogenic activities of these compounds suggest the extended phenotype of *Massospora* that modifies cicada behavior to maximize dissemination is chemically-induced.
What makes a zombie ant tick? An integrative approach to understand fungus-induced behavioral manipulation

WED 4

Charissa de Bekker
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Abstract

Certain fungal entomopathogens have evolved to adaptively manipulate their host’s behavior as a strategy to increase transmission. One enigmatic example are the fungi within the complex *Ophiocordyceps unilateralis* that infect and manipulate ants of the tribe Camponotini. Infected ants are made to leave the nest and latch on with their mandibles at elevated positions to facilitate spore dispersal. We use an integrative approach to unravel how these fungi are able to establish the altered ant behaviors we observe. Studies that range from -omics approaches and forward genetics, to behavioral analyses and ecological surveys are moving us closer to understanding how *Ophiocordyceps* fungi alter the behavior of their ant hosts. We ask is what effectors these fungi secrete to manipulate ant behavior and how these effectors impact the ant pathways involved. We address this question with controlled infection experiments followed by behavioral analyses and comparative mixed transcriptomics. This work is resulting in candidate manipulation compounds that we aim to further characterize using forward genetics. We also ask how seasonal and daily fluctuations in light, humidity and temperature contribute to the disease dynamics of *Ophiocordyceps*-ant systems. Field studies demonstrate that manipulated biting behavior is centered around solar noon and suggest that illumination levels form an important factor for ant cadaver placement and fruiting body development. Moreover, transcriptomics data show daily fluctuations in *Ophiocordyceps* gene expression in cultures entrained by light. Combined, these approaches will reveal ultimate and proximate drivers involved in fungal manipulation of ant behavior.
A different fungus in every pocket: unexpected symbiont diversity and mycangium diversity suggest symbiont switching in the ambrosia beetle tribe Xyloterini

WED 5

Chase Mayers¹, Thomas Harrington¹, Douglas McNew¹, Richard Roeper²

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Abstract

Adult ambrosia beetles carry co-adapted fungal cultivars (ambrosia fungi) in storage organs called mycangia, which occur in various body parts and vary greatly in complexity. In general, ambrosia fungus clades in the Ceratocystidaceae (Microascales) radiated after the evolutionary origin of their associated mycangia, and these mycangium-cultivar combinations have remained stable through evolutionary time. However, the symbioses of the ambrosia beetle tribe Xyloterini were understudied. We collected representatives of the three Xyloterini genera and characterized their mycangia and mycangial symbionts. As reported earlier, Trypodendron consistently yielded ambrosia fungi in the genus Phialophoropsis, including three new putative species, though some fungal species were shared among beetle species. Unexpectedly, mycangia of the previously-unstudied Indocryphalus pubipennis are smaller and differently-shaped than Trypodendron mycangia, and they carry a different genus of Ceratocystidaceae: Toshionella, which are the ambrosia fungi of Asian Scolytoplatypus (Scolytoplatypodini), many of which are sympatric with I. pubipennis. Xyloterinus politus was known to have two different types of mycangia with uncharacterized symbionts. A new putative species of the ubiquitous ambrosial genus Raffaelea (Ophiostomatales) was found in the paired oral mycangia of both sexes, and a new putative genus and species with affinity to the Ophiostomatales was found in the reduced prothoracic mycangia of females. These findings suggest that de novo symbioses and ancient horizontal transfers were associated with morphological changes in mycangia in the Xyloterini. This further supports the theory that developments of novel mycangium types are critical events in the evolution of ambrosia beetles and their co-adapted fungal mutualists.
Abstract

The increasing genomic resources of entomopathogenic fungi have advanced our knowledge regarding fungal biology and their interactions with insect hosts in the last decade. However, our understanding of the insect commensal fungi still lagged behind with little genomic information, especially for the early-diverging lineages, like Harpellales (Kickxellomycotina, Zoopagomycota). Harpellales are common fungal endobionts associated with digestive tracts of immature aquatic stages of various Diptera, including black flies, midges, and mosquitoes. Harpellales have been estimated to have an ancient origin with their Diptera hosts. Their long-term association may have left genomic hallmarks that deserve careful examination. We have sequenced and annotated nine whole-genome sequences of Harpellales fungi and conducted the first comparative genomics within the order as well as with entomopathogenic ones across the fungal tree of life. Harpellales genomes feature low GC content (26-37%) and present large genome size variations (25-102 Mb). We identified a gene toolbox presumably essential to the fungus-insect symbiosis, which is utilized by both insect-pathogenic fungi (Ascomycota and Zoopagomycota) and commensals (Harpellales) but absent in free-living relatives (Kickxellomycotina). Our results not only narrowed the genomic scope of fungus-insect interactions from several thousand genes to eight core players but also distinguished host invasion strategies employed by insect commensals and pathogens. The genomic content suggests that insect commensal fungi rely mostly on adhesion protein anchors that target the digestive system of insects, while entomopathogenic fungi maintain more transmembrane helices, signal peptides, and pathogen-host interaction genes to inactivate the host inflammation system and suppress the host defense.
Potential new reservoir hosts: a study with *Ophidiomyces ophiodiicola* and *Nannizziopsis guarroi*

WED 7

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Abstract

*Ophidiomyces ophiodiicola* and *Nannizziopsis guarroi* are fungal pathogens responsible for devastating and often fatal infections in reptiles. *O. ophiodiicola* is the primary agent of snake fungal disease and an emerging infectious disease. *N. guarroi* is often associated with fatal epidermal infections in lizard species, for example veiled chameleons and iguanas. Because other fungal diseases, including white nose syndrome and chytridiomycosis, are causing extreme declines in wildlife biodiversity, we are concerned about the potential for *O. ophiodiicola* to spread to naïve populations and its ability to infect hosts other than snakes. Prior to our experiment, we completed the University of Wisconsin-Madison institutional animal care and use committee (IACUC) regulations. We then conducted an infection trial using 12 adult corn snakes and 12 juvenile bearded dragons, species chosen because of their close phylogenetic relationship to one another. Our experiment involved a cross inoculation using one strain of *O. ophiodiicola* and one of *N. guarroi* each given to a group of corn snakes and a group of bearded dragons. As expected, *O. ophiodiicola* caused visible infection in snakes, but not in lizards. Similarly, *N. guarroi* caused visible infection in lizards (fulfilling Koch’s postulates), but not in snakes. However, after animals were euthanized, we placed excised skin pieces on dermatophyte test medium, and discovered each pathogen was able to colonize the skin irrespective of host species. Our results suggest that both snakes and lizards are potential reservoir hosts i.e. hosts that can maintain the fungus without becoming infected.
Looking for truffles: exploring symbiotic mycophagy in two birds endemic to Patagonia

WED 8

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¹University of Florida, Gainesville, USA. ²Universidad Austral de Chile, Valdivia, Chile

Abstract

Ectomycorrhizal fungi play key roles in forests by feeding nutrients to the roots of trees in exchange for sugars. Some of these fungi form underground mushrooms called truffles that rely on animals for spore dispersal. Most truffles produce strong odors to attract mammals which dig them up, eat them, and spread the spores in their feces. Temperate rainforests of southern South America are dominated by Nothofagaceae trees that depend on truffles for nutrients, but mammals are relatively scarce and truffles in this system do not produce strong odors. However, the truffles resemble fruits, suggesting that they are dispersed by animals that eat fruit and rely on sight rather than smell to find food. The objective of this study is to document the symbiosis between two understory birds: Chucao Tapaculo (Scelorchilus rubecula) and Black-throated Huet-huet (Pteroptochos tarnii) and several species of endemic truffle fungi in Nothofagaceae forests. We documented the diet of the birds by microscopically and molecularly analyzing fecal samples. Standard microscopy methods were used to confirm, identify, and quantify spores in the fecal samples. We used high-throughput amplicon sequencing (HTS) to identify fungi by sequencing ITS and LSU. Our HTS results confirmed the presence of at least 29 ectomycorrhizal fungi in the fecal samples, including nine truffle-like fungi. Some taxa detected are Cortinarius (Thaxterogaster) sp., Descolea brunnea, Melanogaster sp., Hysterangium sp., Ruhlandiella patagonica and Cystangium nothofagi. These results suggest a putative case of avian mycophagy where both chucaos and huet-huets eat truffle-like fungi and disperse spores.
Heart Rot Hotel 2: a synthesis of the symbioses between fungi and woodpeckers across North America

WED 9

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Abstract

Fungi, woodpeckers, and tree cavities are intricately entwined. Historically, studies of these relationships relied upon visual observation of fungal fruiting bodies, tree decay class categorization, and limited culturing work. These methods provided some insights, but left fundamental questions about woodpeckers and fungi unanswered. How many fungi are associated with woodpeckers? How common and widespread are these relationships? Do woodpeckers facilitate fungal dispersal, or do they select trees with certain fungal inhabitants? High-throughput amplicon sequencing (HTAS) provides more accurate and effective characterization of the fungi associated with tree cavities and woodpeckers. Here we use HTAS to study the fungal communities associated with woodpeckers across North America, covering a range of ecologies and management needs. First, we compared the symbiotic relationship between endangered red-cockaded woodpeckers and fungal communities in pines of the Southeastern United States, to relationships between acorn woodpeckers and fungi in oaks of California. We then looked across fungal communities in cavities excavated by four additional woodpecker species in the Pacific Northwest. We saw a similar pattern across different birds and ecosystems – trees with cavities excavated by woodpeckers have fungal communities that are distinct from fungal communities in trees without excavations. Some woodpecker species appear to select trees with certain fungi for excavation, others facilitate fungal dispersal during excavation, and some do both. Taken together, these results illustrate that associations between woodpeckers and fungi are widespread among species, geography, and ecoregions. These data serve as a first step towards answering larger-scale questions about global associations between woodpeckers and fungi.
The mycobiome of bats: Critical information for understanding and managing white-nose syndrome

WED 10

Daniel Lindner\textsuperscript{1}, Michelle Jusino\textsuperscript{2,1}, Jonathan Palmer\textsuperscript{1}, Mark Banik\textsuperscript{1}, Paula Marquardt\textsuperscript{3}, Deahn Donner-Wright\textsuperscript{3}

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Abstract

Since first documented in 2006, white-nose syndrome (WNS) has caused massive declines in bat populations throughout eastern North America. Caused by the fungus \textit{Pseudogymnoascus destructans} (Pd), WNS offers an opportunity to examine the fungal associates of bats and to determine how mycobiomes may influence both disease development as well as the outcome of potential WNS treatments. We used high through-put amplicon sequencing (HTAS) of the fungal ITS region to characterize baseline mycobiomes of little brown bats (\textit{Myotis lucifugus}) from multiple locations spanning WNS-positive and -negative geographic regions. We determined the Pd load on the bats via qPCR. We examined the effects of site, sex, and Pd load on mycobiomes and identified the taxa associated with these variables. Preliminary analyses suggest site and disease status most strongly influence the mycobiome of little brown bats. Next, we conducted a treatment trail on Pd positive bats using UV-C light and tracked mycobiomes on treated and untreated animals. Pd is extremely sensitive to UV-C light compared to other microorganisms, thus raising the possibility of being able to selectively alter the mycobiomes of bats to minimize WNS with little disturbance to the overall fungal community. Following UV treatment, little change was observed in the overall mycobiome, despite reduced levels of Pd in UV-treatment groups, suggesting that it may be possible to use UV-light to combat WNS without altering the overall mycobiome.
Phylogenetic reconstruction of the Laboulbeniomycetes

WED 11

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Abstract

The class Laboulbeniomycetes (Ascomycota, Pezizomycotina) comprises fungi that are obligately associated with Arthropoda as biotrophs or for dispersal. Three orders are recognized, Herpomycetales, Laboulbeniales, and Pyxidiophorales. In addition, the genera Chantransiopsis, Coreomycetopsis, Laboulbeniopsis, and Tetrameronycha have not been formally placed because of lack of sequence data and undersampling – resulting in the absence of many families and genera in analyses. Owing to difficulties in DNA extraction and PCR amplification, molecular phylogenetic studies of the class lag behind other groups of Ascomycota. Recent advances include improved DNA isolation techniques, the incorporation of whole-genome amplification prior to PCR, and the design of Laboulbeniomycetes-specific primers. These have led to an increase in sequence data, mostly for the nuclear ribosomal loci, but also other regions, such as the mitochondrial SSU and MCM7. We DNA barcoded species to test hypotheses about speciation; we formally described a new order using multi-locus inferences and molecular clock analyses; and we identified 4–5 large clades within Laboulbeniomycetes that might correspond to orders based on the small subunit (SSU) rRNA gene. Here, we expand on these studies by presenting a phylogenetic reconstruction of the class using all available SSU and large subunit (LSU) rRNA gene sequences and making recommendations for future work.
The ecology and evolution of animal associations in Hypocreales, a synthesis of phylogenetic datasets across the order.

WED 12

Ryan Kepler
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Abstract

Phylogenies derived from multilocus datasets have revolutionized fungal taxonomy and our understanding of diversity. The proliferation of these analyses over the fungal tree of life have paid dividends in two significant areas: understanding the evolution of fungal traits and the inference of species present in samples where they are unable to be directly observed. Fungi in the order Hypocreales form interactions with organisms across the tree of life, playing roles ranging from symbionts to pathogens. Furthermore, some species defy easy trophic classification, occupying multiple niches opportunistically. These interactions are important for ecosystem function across natural landscapes. Additionally, the pathogen diversity in Hypocreales has contributed important biocontrol agents of insects, nematodes and plant diseases. Despite their ecological significance, we are only at the beginning of understanding complex hypocrealean life-histories, a knowledge gap that has limited our ability to leverage them in meeting society’s needs. The degree to which hypocrealean fungi are able to utilize divergent nutritional sources (e.g. plant symbiont vs. insect pathogen vs. saprobe) potentially set the stage for future adaptive shifts in host association or substrate specialization. This talk explores the evolution of life histories in Hypocreales using a multilocus dataset derived from phylogenetic work across the order, and uses that as a guide to identify and understand species distributions from environmental sampling.
Phylo-secretomics of zygomycete fungi: “fungi are what they secrete”

WED 13

Joey Spatafora, Ying Chang, Yan Wang, Jericho Ortiz, Derreck Carter-House, Gerald Benny, Matthew E. Smith, Nicole Reynolds, Timothy Y. James, Wiiliam Davis, Kevin Ames, Igor Grigoriev, Jason E. Stajich

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Abstract

Phylogenomic analyses of fungal species with known ecologies have revealed considerable insight into the genomic evolution associated with different ecologies and nutritional modes (e.g., mycorrhizae, wood decay, etc.). These analyses have been conducted primarily among species of Dikarya with well characterized ecologies. Fungi of Mucoromycota and Zoopagomycota comprise diverse lineages of fungi that were formerly classified as zygomycetes and their ecologies are frequently less characterized compared to Dikarya. Mucoromycota shares a most recent common ancestor (mrca) with Dikarya, and its ecologies tend to be plant-associated or decomposers of plant materials. Meanwhile, Zoopagomycota is a sister group to the Mucoromycota-Dikarya clade and its ecologies tend to be animal- or fungal-associated. In both phyla, however, there exist numerous species with divergent and/or poorly characterized ecologies. As part of the ZyGoLife research consortium we have sequenced more than 100 reference genomes and 400 low-coverage genomes of Mucoromycota and Zoopagomycota to advance our understanding of the phylogenetic history and genomic evolution of these fungi. We are using these data to predict the secretome as proxies for their ecologies and nutritional modes. We will report on phylogenomic analyses of Mucoromycota and Zoopagomycota genomes, patterns associated with known ecologies of the phyla, and extrapolations to unknown ecologies or nutritional modes within the phyla. This research will inform our understanding of the relationship between genome content and the independent transitions to common life styles across the Kingdom Fungi.
Reshaping our understanding of “rare” fungi: phylogenomic analyses of the Kickxellales demonstrate additional diversity

WED 14

Nicole Reynolds¹, Gerald Benny¹, Jason Stajich², Derreck Carter-House², Kerrie Barry¹, Igor Grigoriev³, Matthew Smith¹

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Abstract

Despite being among the earliest lineages to adapt a non-flagellated, filamentous growth form, species within the phylum Zoopagomycota remain understudied and incompletely characterized. The Zoopagomycota includes diverse species of mycoparasites, endo- and ectoparasites of small animals (e.g. nematodes, amoebae), insect endobionts, and saprotrophs. Saprotrophic species are recognized within the subphylum Kickxellomycotina (Kickxellales) and are closely related to insect gut-associated fungi known as trichomycetes. Although most species are apparently uncommon, Coemansia species are among the most frequently encountered Kickxellales and can be cultured from soil or dung. The members of other Kickxellales genera are rarer, with some known only from a single isolate (e.g. Myconymphaea yatsukahoi). Phylogenetic analyses and molecular data are limited for the Kickxellales, due in part to the difficulties with culturing these fastidious fungi. Despite being putatively saprotrophic, some Kickxellales are slow growing, easily contaminated with other fungi, and require specific temperatures or nutrients for optimal development. Furthermore, Coemansia species co-occur with bacteria that are resistant to various antibiotics and the increased fungal growth in some of these co-cultures suggests a potential symbiotic association with bacteria. For this project we grew strains of Coemansia and relatives and used Illumina for low-coverage genome sequencing. From these data we reconstructed a robust phylogeny that illustrates the diversity of Coemansia and recovers the relationships between taxa within the Kickxellales. We were also able to mine the sequencing data for information on the potential bacterial communities associated with Coemansia species and generate hypotheses regarding their interactions.
Evolution and comparative genomics of zygomycete fungi

WED 15

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Abstract

Zygomycetes comprise substantial biodiversity of fungi inhabiting saprotrophic, symbiotic and pathogenic niches. They are so-called “early-diverging” fungi that are diverged from a flagellated ancestral fungus and are sister lineages to terrestrial Dikarya fungi. Phylogenetic analyses of whole genome sequences have supported the paraphyly of zygomycete fungi which are now classified into two phyla: Mucoromycota and Zoopagomycota. Mucoromycota includes three subphyla (Glomeromycotina, Mortierellomycotina, and Mucoromycotina) which have coenocytic hyphae and are typically plant-associated fungi (mycorrhizal, endophytes, and decomposers). The subphyla within the Zoopagomycota are the Entomophthoromycotina, Kickxellomycotina, and Zoopagomycotina, most of which have animal-associated (symbionts or pathogens) or mycoparasite ecologies. Phylogenetically, Mucoromycota is the sister lineage to Dikarya and Zoopagomycota is sister to the clade of Mucoromycota and Dikarya. We have generated 146 reference quality genomes across the six subphyla of zygomycete fungi and use these data to compare genomic diversity, identify lineage-specific genes, and test for evolutionary patterns of gene family gains and losses along the lineages. We will describe research progress on the phylogenomics and comparative genomic content of the zygomycete fungi to shed light on the animal, plant, and mycoparasite symbiotic and saprotrophic lifestyles.
Macronovolutionary analyses of fruiting body forms and nutritional modes in Agaricomycetes based on an 8500-species phylogeny

WED 16

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Abstract

The Agaricomycetes contains approximately 35,000 described species and a wide variety of fruiting body morphologies such as resupinate, coralloid/clavarioid, pileate-stipitate, sessile and gasteroid forms, as well as diverse nutritional modes, such as saprotrophy, parasitism and mutualistic symbiosis. Previous studies have hypothesized that the corticioid fruiting body form is plesiomorphic, there is a directional trend that favors pileate-stipitate forms, the gasteroid form is irreversible and pileate-sessile and clavarioid forms are labile. We reconstructed a five-gene phylogeny that contains 8,500 species of Agaricomycetes in order to identify broad evolutionary patterns within this group, and to test the following hypotheses: (H1) Resupinate forms are plesiomorphic; (H2) Pileate-stipitate forms promote diversification; (H3) The evolution of gasteroid forms is irreversible; (H4) The ectomycorrhizal (ECM) symbiosis promotes diversification. We estimated trait-independent diversification rates, as well as trait-dependent diversification rates using state speciation and extinction (SSE) models. We tested several coding regimes that include transitions from non-gasteroid to gasteroid forms, and multi-state transitions such as resupinate, clavarioid, pileate-stipitate, sessile and gasteroid. Our results suggest that the ancestor of Agaricomycetes was a saprotroph with a resupinate fruiting-body and at least 478 morphological transitions have occurred. Pileate-stipitate forms have higher diversification rates than all other forms and saprotrophic clades have slightly higher diversification rates than ECM lineages. However, certain ECM clades exhibit higher diversification rates than their non-ECM sister clades, indicating that this switch in nutritional mode may promote diversification at local phylogenetic scales.
A global approach to informing the Pezizomycotina tree of life via endophytic fungi: phylogenetic integration of genomic, symbiotic, environmental, and physiological data layers

WED 17

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Abstract

The Pezizomycotina represent the most species-rich subphylum of fungi and encompass an enormous range of ecological roles. Prevalent among these is endophytism, an ancient, widespread, and ecologically important symbiotic association with photoautotrophs that likely arose in the stem lineage of Pezizomycotina ca. 590-467 Ma. Endophytes are especially diverse in the Pezizomycetes and Leotiomyceta, complementing the lichen-forming fungi and representing dynamic evolutionary and ecological boundaries with pathogens and saprotrophs. Our multidisciplinary team is working to (1) enrich the Pezizomycotina genealogy of life by collecting endophytic fungi and their hosts in biodiversity hotspots worldwide; (2) evaluate endophyte diversity and distributions via culture-based and culture-free surveys; (3) develop informatics tools to create a field-to-genome pipeline for improving the phylogenetic backbone for Pezizomycotina and rapidly pinpointing new lineages for taxonomic identification; (4) test hypotheses regarding fungal-photobiont interactions in symbio; and (5) integrate diverse data layers from genomic, symbiotic, environmental, and physiological pipelines with the enriched Pezizomycotina phylogeny, illuminating the evolutionary history and trajectory of the lineage as a whole. Here we will highlight key results of this multifaceted project, describing insights into the ecology and evolution of Pezizomycotina via the lens of fungal-photoautotroph interactions. We will discuss emergent perspectives on endophyte diversity and host use; the complementarity of culture-free and culture-based approaches; and how data integration in the context of new computational and bioinformatics tools enables the rapid coalescence of data streams for fungal systematics and ecology,
fostering new hypotheses about evolutionary, ecological, and symbiotic dynamics in the most diverse subphylum of fungi.
Spatiotemporal variation in dust-associated fungi and bacteria along an elevation gradient in California’s Sierra Nevada Mountains

WED 18

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Abstract

Dust provides exogenous inputs of nutrients, especially in slowly-eroding, depleted ecosystems where weathering intensity may limit nutrient inputs from underlying bedrock. One important, yet often overlooked, aspect of dust is its functional role as a vector for microbial dispersal. Although we know little about the role of dust-associated microbial dispersal in terrestrial ecosystem functioning, dust-driven nutrient and microbial inputs may have transformative effects on ecosystems far from where they were derived or evolved. Using high throughput molecular techniques, paired with isotopic and nutrient analyses, we examined spatiotemporal variation in dust-associated microbial communities as exogenous inputs along an elevation gradient within California’s Sierra Nevada. Previous findings show that dust comes from a combination of Central Valley and Gobi Desert sources, and that it brings as much phosphorus (P) is is generated from newly weathered bedrock. We found that both the provenance and the microbial community differ across space and time. Both fungal and bacterial community composition and the functional capacity of these communities differed by elevation, month in the dry season, and year. Fungal pathogens in particular were more diverse in the lower three than the highest elevation. We also found high representation of both cyanobacteria and algae in dust relative to soil communities. Our work along this elevation gradient in the Southern Sierra Critical Zone Observatory reveals variable nutrient and microbial inputs from both regional and transoceanic dust sources.
How fire and other environmental drivers influence soil fungal communities in prairies of the Pacific Northwest

WED 19

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Abstract

Extensive prairies were maintained by native American burning in the Pacific Northwest for about 10,000 years, and today increasingly prescribed burning is a management tool for restoring prairies. However, the effects of fire on soil fungal community composition in prairies in unknown. We examined soil from prairies in Washington and Oregon that included a fire chronosequence: burned within one month, within two years, and not burned in approximately 150 years. The total fungal communities were distinct by region and site, and there were small but significant effects of fire. Analysis of functional groups revealed stronger fire effects. All but two genera of arbuscular mycorrhizae, most of the ectomycorrhizae, and a few plant pathogens and saprotrophs responded to fire. Time since burning mattered; AMF community composition differed among burning intervals with some genera only found in certain burning treatment plots. For example, the AMF genus Dominikia was only found in recently burned treatment plots, while Funneliformis was only found in plots not burned within 150 years. Because some fungi were favored by short fire intervals and others were not, future management should consider the consequences of fire for individual taxa of interest such as pathogens and mycorrhizae when planning burning intervals.
Mapping the distribution of emerging pathogen *Coccidioides immitis* using one health surveillance in Washington State

WED 20

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Abstract

Surveillance for *Coccidioides* in Washington contributes to the understanding of public health risk and habitats for pathogen persistence. A One Health approach to *Coccidioides* surveillance includes performing follow-up exposure investigations for human and animal cases, environmental surveillance based on niche model predictions, and canine serology surveys as a proxy method for estimating geographic areas of increased risk. In 2015 and 2016, soil samples collected for two exposure investigations in Benton County tested positive for *Coccidioides* DNA. Environmental surveillance between 2015 and 2018 was performed in Benton, Kittitas, Walla Walla, and Yakima Counties with over 500 samples collected from 11 localized sites chosen based on niche modeling of soil characteristics compared to Southwest endemic regions. Environmental surveillance yielded positive detections of *Coccidioides* from five localized sites, three of which are in Yakima and Kittitas Counties, where *Coccidioides* has not previously been reported from soils. Canine serology surveys were conducted in collaboration with 25 veterinary clinics in 17 counties between 2014 and 2018. Over 1200 canine serum samples were collected and tested for presence of *Coccidioides* IgG antibodies. Serology results indicate an average of 8% of canines sampled in Washington have been exposed to *Coccidioides*, with the majority of positive canines coming from Benton, Franklin, Yakima, and Walla Walla Counties. Considering these additional environmental detections and canine serology data, it is likely that *Coccidioides* presents a risk to humans and animals across a larger region of central Washington than previously described and highlights a need for continued environmental surveillance.
Community Composition and Structure of Submerged Detritus Inhabiting Fungi Across Temperate Peatland and Stream Habitats

WED 22

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Abstract

We examine species distributional patterns within a phylogenetic framework to refine our understanding of temperate peatland and alkaline stream fungal communities, species distributional patterns, and provide a robust framework to elucidate how major groups of fungal taxa are distributed across multiple habitats. Using both culture-dependent and culture-independent techniques, we examined how habitat, geography, and phylogeny influence the structure of detritus-inhabiting fungal communities. Results indicated that all sites contain numerous unidentified, abundant taxa but that stream communities contain more species, have greater phylogenetic diversity, and possess greater phylogenetic distinctiveness as compared to peatlands. In addition, analysis of the nine most abundant fungal classes indicated that phylogenetic clustering was more prominent within peatland habitats as compared to stream habitats. Lastly, site variation had the greatest impact on community structure, followed by habitat, and region. This research allows for the integration of additional ecological, functional and phylogenetic information further refining our understanding of fungal community ecology.
The influence of long-term glyphosate use on fungal community composition and decomposition capabilities

WED 23

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Abstract

Glyphosate is the most widely used herbicide worldwide. This organophosphorus pesticide inhibits essential aromatic amino acid biosynthesis in plants, a metabolic pathway shared by bacteria and fungi. Unlike bacteria, fungal glyphosate effects are not well-studied. Published data vary by taxon, are often contradictory, and research has historically focused on agricultural environments. Soil-inhabiting fungi are important decomposers of carbon compounds, especially wood. Understanding changes in decomposition will become increasingly important as we move toward a carbon economy. High-throughput sequencing data on fungal community response to glyphosate would be useful, but are lacking. The effect of glyphosate on wood decay, an essential ecosystem service primarily performed by basidiomycetes, has received little attention. To explore this, we asked “does repeated, long-term glyphosate application impact soil and wood fungal communities?” and “does glyphosate exposure alter wood decay processes?” Southern pine sapwood stakes were placed into soil using a matched-pair plot design (glyphosate/no glyphosate) with four blocks at each of three sites. Destructive harvests were planned every six months for five years. At each sampling: (1) eight stakes/plot were visually rated for decay progression and returned; (2) two soil samples, before and after glyphosate application, and one stake were collected for fungal community analysis of the ITS2 region using Illumina MiSeq. The sequence data will fill a knowledge gap regarding shifting fungal communities. Coupling these data with a specific ecosystem function (wood decomposition) will help gain a deeper understanding of the functional influence of targeted taxa and glyphosate impact on the system.
Trophic skew in belowground fungal communities of cultivated coffee and native Rubiaceae

WED 24

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Abstract

Trophic skew, the tendency for invasions to predominate at lower and extinctions at higher trophic levels, has rarely been examined outside of aquatic systems. Because fungi act as primary consumers (saprotrophs, plant pathogens, endophytes) and as secondary consumers (animal pathogens, mycoparasites), trophic skew in terrestrial fungal communities has implications for key ecosystem processes, including nutrient cycling and fungal disease regulation. Here we present two metabarcoding studies using the ribosomal DNA ITS2 region and FUNGuild to characterize root fungal communities of conventionally-managed and organic coffee, and coffee compared with naturally-occurring relatives in the Rubiaceae in adjacent forests at three sites in Monteverde, Costa Rica. Trophic structure of root fungal communities differed between conventionally-grown and organic coffee. Organic roots harbored a greater diversity of saprotrophs, plant pathogens and potential mycoparasites than conventional ones, while fungi with the potential to act as saprotrophs and plant pathogens were overrepresented in conventional coffee. Trophic structure also differed between root fungal communities in coffee and those in relatives of coffee in the forest understory. Saprotrophs, root endophytes and possible mycoparasites were detected at a higher frequency in forest than in coffee. In contrast, fungi with the potential to act as plant pathogens or as saprotrophs were detected more frequently in coffee. Taken together, these results suggest that conventionally-managed coffee root fungal communities are not only less diverse than their forest and organic counterparts but also enriched in some primary consumer guilds and depauperate in the fungi most likely to control plant fungal disease.
Metagenomic study of soil fungal communities associated with Southern hemisphere exotic pine forests

WED 25

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Abstract

Centuries of planting exotic pine forests across the southern hemisphere have been accompanied by co-introduction of their obligate symbiotic ectomycorrhizal fungi (EMF). Species diversity of these exotic EMF communities is often greatly reduced relative to their native pine forest communities in the northern hemisphere. Analysis of ITS metabarcode sequences from soil samples collected across Australia and New Zealand reveals that soil fungal communities growing under exotic pine plantations are enriched by the addition of a limited number of pine-associated EMF which exhibit novel biogeographic patterns arising from different historical patterns of introduction and plantation forestry. Using multi-locus DNA barcoding of field-collections and herbarium specimens, we traced the geographic origins and distribution of over one dozen species of EMF co-introduced with exotic pines to Australia and New Zealand. These studies provide insight into the biogeography of EMF introductions associated with exotic pines, and the role of EMF in facilitating invasion by pines.
The mycoflora of Mexico

WED 26

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Abstract

Mexico may have up to 200,000 species of fungi. However in the national catalog of fungi, assembled ca. ten years ago by the Comisión Nacional Para el Conocimiento y Uso de la Biodiversidad (CONABIO), a Mexican government agency, only 2,300 species were recorded. A preliminary check-list for North American nonlichenized fungi, assembled with specimens data from fungaria located in Canada, United States and Mexico, reported up to 5,000 species in Mexico. This list had a number of caveats regarding orthographic errors, unsolved synonyms, and in its current version, it does not provide information regarding distribution or details on classification.

In order to provide a comprehensive catalog of fungi from Mexico, we assembled a database of 8,882 records of 6,359 taxa, including 6,010 species and 349 taxa below species rank. Specimens records were retrieved from the database of the National System of Biodiversity Information (SNIB in spanish), hosted and maintained by CONABIO, and from peer-reviewed publications, and other relevant bibliographic sources.

The results indicate that Basidiomycota accounts for 57.8\% of the species, and Ascomycota represents 38.2\%. In contrast, 53.6\% of the 297 families known from Mexico belong to Ascomycota, and 38.7\% to Basidiomycota. Veracruz (at the Gulf of Mexico) is the state with the highest number of species recorded (1144). Since 1970 mycological knowledge has increased rapidly in Mexico, with an impasse between 1982 and 1997, probably related with the economic crisis over that period.
**Allodus prostii** comb. nov., causal agent of tulip rust

**WED 27**

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**Abstract**

During surveys of the rust fungal flora in Pakistan samples of *Puccinia prostii* infecting *Tulipa clusiana* were collected for study. Our phylogenetic and morphological analyses showed that this taxon is congeneric with the genus *Allodus*. On the basis of these results the new combination, *Allodus prostii* comb. nov. is proposed and the species is fully described and illustrated. Members of the genus *Allodus* may now be distinguished from *Puccinia* species by the lack of a uredinial state, production of conspicuous spines on the teliospores, and autoecious life cycle.
Development of a machine learning-based mushroom app for real-time image classification

WED 28

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Abstract

Of the thousands of mushroom species in North America, many are highly prized edibles, and a few are poisonous. Most mushroom poisonings stem from misidentification and consumption of a toxic mushroom mistakenly believed to be edible. Accurate mushroom field identifications rely on several morphological traits to discriminate between taxa, and on an understanding of how mushroom growth and development changes through time, climates, and environments. Here we report the development of a machine learning-based mushroom classification app called Purdue University Mushroom App (PUMA). We used Google’s tensorflow for poets version 2 to develop the standalone app. First, the identity of hundreds of images available on the internet of different angles and developmental stages for each genus were verified. These images were then fed into tensor flow training and resulted in classification models called graphs. These graphs were then transported into mobile handsets and images from the camera view finder were classified in real time. As a proof-of-principle, our app was trained on a dataset of Gyromitra and Morchella species, and then tested. For initial tests, 20 known images that were not used in training session were challenged against the app. The app returned the correct diagnosis of Gyromitra in all test cases (100% sensitivity, and 90% specificity), and a correct diagnosis of Morchella in all but one test cases (90% sensitivity and 100% specificity). Our next step will be expanding our database into other common genera such as Amanita, Agaricus, Tricholoma, and Cantharellus.
The Rice Blast Fungus and Allied Species: A Monograph of the Fungal Order Magnaporthales

WED 29

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Abstract

Magnaporthales (Sordariomycetes, Ascomycota) includes economically and scientifically important cereal and grass pathogens, such as the rice blast fungus *Pyricularia oryzae* (syn. *Magnaporthe oryzae*), the take-all root rot pathogen *Gaeumannomyces graminis*, and the turfgrass summer patch pathogen *Magnaporthiopsis poae*, as well as endophytes and saprotrophs. We recently created and released an e- monograph website of Magnaporthales via Rutgers University (https://magnaporthales.sebs.rutgers.edu). All accepted species names in Magnaporthales are included. On the basis of literature and specimen examination, species description, diagnostic illustration, type designation, host range, geographical distribution, and literature are provided for representative taxa, especially the type species for each genus. Genbank sequence accession numbers of eight genes including ITS, 18S, 28S, *ACT*, *CAL*, *MCM7*, *RPB1*, and *TEF1* also are provided in the e-monograph. Genomic sequences of 24 representative taxa are hyperlinked to the genome databases in FunGI (http://dblab.rutgers.edu/FunGI/index.php) and the Broad Institute (ftp://ftp.broadinstitute.org/pub/annotation/fungi/magnaporthe/ genomes). Four dichotomous keys to three families and 32 genera, and keys to species of three genera are provided. Our website is searchable, and links species name to related data and other information. The Magnaporthales e-monograph provides free access on updated taxonomic, biogeography and molecular data to researchers and the broader user communities worldwide, which will facilitate their work on systematics, biodiversity, evolution, genetics, plant protection and quarantine.
Target capture of ultraconserved elements from four classes of lichenized Ascomycota – targeting the fungal symbionts for phylogenomic inference

WED 30

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Abstract

Variation in phylogenetic signal for a given locus across the Ascomycota is likely driven by the long evolutionary history of the phylum, spanning several hundred million years. This disparity in phylogenetic signal has led to a patchwork of markers being employed for resolving relationships across the Ascomycota and limiting the combinability of data from independent studies. This is, in part, being addressed by large-scale genome sequencing projects, like JGI’s 1K Fungal Genomes Project. However, the scale and scope of diversity in the Ascomycota means that alternative approaches will be required to harness the power of genomics to provide insight into evolutionary relationships for both deep- and shallow-scale studies. We designed a set of sequence capture probes to target over 1800 ultraconserved loci (UCEs) across the Ascomycota. In order to assess the utility of these probe sets for collecting phylogenomic data from divergent taxa, we sampled lichen species sharing a MRCA approximately 300 mya and representing 4 classes, 15 orders, 33 families, and 56 genera, including 6 congeners and 2 conspecifics. We captured 1650 loci with a range of 31 to 824 (mean of 434) per sample. We also extracted orthologous loci from publicly available genome sequences representing all major lineages within the Ascomycota. The resulting phylogeny is strongly supported at most nodes and is consistent with phylogenies estimated from smaller multi-locus datasets. These results illustrate the reliability of the phylogenetic information contained in ascomycete UCEs and represent a novel approach towards collecting genomic data from a community of symbionts.
Xylariales of the Boston Harbor Islands

WED 31

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Abstract

The Xylariales (Sordariomycetes, Ascomycota) is an order of mostly stromatic perithecial fungi generally inhabiting wood and other plant debris, as well as some important plant pathogenic species. As follow-up to an extensive fungal inventory conducted between December 2012 and May 2017 at the Boston Harbor Islands National Recreation Area (BHI) in Massachusetts (Haelewaters et al. 2018), members of the Xylariales were examined in detail, including new collections. A new name, Xylaria finismundoensis, is proposed; this taxon provides the first evidence of a saprotrophic lifestyle for members of a Xylaria clade previously only known as endophytes. We utilize important taxa in the Xylariales from the Boston Harbor Islands to illustrate facets of the the evolutionary history and ecology of Xylarialean fungi, providing a brief overview some commonly collected families in the order (Xylariaceae, Hypoxylaceae, Graphostomataceae, Lopadostromataceae, and Diatrypaceae).
Leafing out the tree from top to bottom: morphological, taxonomic and phylogenetic investigations of insectivorous Oomycota

WED 32

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Abstract

Recent molecular studies have identified a number of early-emerging incertae sedis clades that are mostly marine, holocarpic parasites that evolved before or at the time of the “crown Oomycota.” The most basal of these groups are the Eurychasmales and Haptoglossales which are holocarpic parasites of seaweeds and nematodes. More recently it has been suggested that the Atkinsiellales, another early-emerging group of holocarpic parasites, be included along with the Leptomitales and the Saprolegniales in the Saprolegniomycetes. A number of freshwater parasites of insects have been discovered and described in our laboratory as representatives of incertae sedis and saprolegniomycete groups; however, as their taxonomy was based on morphology alone, their true relationships were not known. Here we report the results of a multigene study using 18S, 5.8S, 28S and COX-2 genes that has allowed us to develop a robust phylogeny for these organisms as well as more recently discovered early-emerging Oomycota. Among these findings: a) three new freshwater members of the Atkinsiellales; b) four new members of the Verrucalvaceae (the most basal family of the Saprolegniales; c) Crypticola (Atkinsiella) entomophaga, a parasite of insect eggs, was once thought to be a member of the Atkinsiellales but is more closely related to the Eurychasmales and Haptoglossales; d) Aphanomycopsis sexualis, a parasite of midge eggs, forms a new monophyletic clade near the cusp of the Saprolegniomycetes/Peronosporomycetes split; and e) Couchia, a eucarpic genus parasitic in midge eggs, forms a recently evolved clade at the apex of the saprolegniomycete lineage.
An insight on the nuclear diversity in a single spore of arbuscular mycorrhizal fungi

WED 33

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Abstract

Arbuscular mycorrhizal (AM) fungi form vital symbiotic relationships with the roots of most plants, and they have been considered key components in the transition from aquatic to terrestrial habitats. A long-standing question in AM research has been whether these coenocytic fungi are homokaryotic or heterokaryotic. Some evidence supports the hypothesis of genetically identical nuclei, while other lines of evidence support the hypothesis of the presence of many divergent nuclei that co-exist within a common cytoplasm. While sexual reproduction has never been observed in AM fungi, several genomic signatures of sexual reproduction have been identified, such as meiosis-specific genes and a putative mating-type (MAT) locus. In addition, it has been shown that some strains can contain two putative MAT alleles and be structured in a homo-dikaryon-like manner. For this study, we sequenced 24 individual nuclei from a single spore of four strains of AM fungi in order to detect whether the nuclei are genetically identical or not. We produced a reference genome for each strain as well as individual nuclei genome assemblies. We performed single nucleotide polymorphism (SNP) analyses across the entire genomes, and we also identified shared regions across each set of 24 nuclei, representing single copy orthologs, in order to quantify genetic variation. Finally, we identified the MAT locus to investigate the co-existence of one or two alleles. Our results show that nuclei within a single spore of these four strains of AM fungi show very low genetic variation, which supports the hypothesis of homokaryosis.
Exploring Foliar Fungal Endophyte Assemblage, Diversity, and Host Specialization in Pine

WED 34

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Abstract

Host specialization of foliar fungal endophytes remains a cryptic and understudied phenomenon. Since patterns of host specialization are sensitive to host taxonomic and spatial scales, a field study that investigates the fungal endophytic community of pines (Pinaceae), a taxonomically well-defined and diverse group, across a wide geographic range spanning much of North America, was conducted. Pines have a high incidence of fungal endophyte infection, likely due to the longevity of their evergreen foliage as well as their dominance in some ecosystems. Furthermore, Lophodermium (Rhytismataceae), a well-studied foliar fungal endophyte genus that is common within pine needles, has high phylogenetic host specificity that is rarely documented in other endophytes. In total, six species from the Pinaceae family were sampled from eight sites across the northeastern United States. Community assemblages of fungal endophytes were analyzed with Illumina MiSeq with a closer investigation of OTUs with high similarity to known Lophodermium sequences. Host specificity of common Lophodermium OTUs were analyzed and compared across geographic and taxonomic groups of pines. These findings will be crucial in furthering our understanding of the evolutionary and ecological nature of these mysterious microfungi on their hosts.
Population genomic insights into the establishment of non-native golden oyster mushrooms (*Pleurotus citrinopileatus*) in the United States

**WED 35**

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**Abstract**

The naturalization of non-native golden oyster mushrooms (*Pleurotus citrinopileatus*) in midwestern and eastern parts of the U.S. represents the first known case of a cultivated mushroom spreading quickly and widely outside of its native range, exhibiting characteristics of invasiveness. The first observations of wild fruitings in American woodlands occurred approximately 7 years ago. Citizen scientist observations have increased significantly over the last two years, with sightings recorded from 9 states so far. To gain insights into the mechanisms behind this species’ introduction and spread, I used population genomic data to test the hypothesis that naturalized golden oyster populations are the result of multiple introductions from cultivation operations. I analyzed genome-wide single-nucleotide polymorphisms (SNPs) from 29 wild mushroom specimens collected in six states, plus 6 commercially cultivated isolates. Clustering patterns revealed by the SNP data are consistent with a larger gene pool of commercial strains from which a limited number of strains differentiated via recombination or mutation. High genetic similarity was found between all wild samples plus two of the commercial isolates examined, suggesting possible source strains linked to wild establishment. Genotypic subdivision of the wild samples does not closely correlate with geographic location, suggesting multiple introductions and human-mediated spread.
Population genomics of toxins between invasive and native ranges of *Amanita phalloides*

WED 36

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Abstract

Toxin producing fungi in the genus *Amanita* (Agaricales, Basidiomycota) are responsible for a majority of mushroom related poisonings worldwide. The most potent of these toxins are the cyclic peptides in *Amanita phalloides*, encoded by the MSDIN family of genes, which inhibit primary metabolism. While the exact role of MSDIN toxins in natural contexts is unclear, their dramatic biological activities make them a compelling focus for studying *Amanita* evolution. Native to Europe, *A. phalloides* has become well-established in its invasive range in California since its introduction in the mid-1900s. Invasive species often evolve in new ranges, a highly understudied phenomenon, and it is likely that the MSDIN genes have evolved in Californian populations. Recently, our laboratory generated 68 genomes of *A. phalloides*: 57 from California and 11 from Portugal. I have developed a bioinformatic pipeline to evaluate the extent of MSDIN gene diversity within *A. phalloides* individuals and how they vary in Californian and European populations. To date, I have found that MSDIN gene composition varies more between individuals from California than they do between Californian and Portuguese individuals. The species in California therefore demonstrates the capacity to synthesize a different repertoire of toxins, suggesting that they are experiencing different selection pressures and may be evolving in their invasive range.
Investigating patterns of HD1 and HD2 mating gene diversity through space and time: insights on how mating system influences invasion and vice versa in *Amanita phalloides*

**WED 37**

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**Abstract**

*Amanita phalloides*, the Death Cap, is an ectomycorrhizal fungus native to Europe and invasive in California (CA), introduced in the last century. Like other Basidiomycotans, *A. phalloides* has a two-locus, tetrapolar mating system, in which mates must have different alleles at both of the loci, i.e. have different mating types. Diversity at these loci is typically extremely high, and many Basidiomycotan species have thousands of mating types. This is believed to be due to negative frequency-dependent selection of novel alleles. Presumably, diversity at mating type alleles was bottlenecked during the introduction of *A. phalloides* to CA.

Here, I examine of alleles of the genes HD1 and HD2, the core self-incompatibility genes of the HD (or A) mating locus, sequenced from 86 *A. phalloides* individuals collected in mapped populations from the invasive range in California as well as across the native range in Europe, with mapped populations from Portugal. The California samples include survey populations that were collected from in 2005, 2014, and 2015, allowing to take a history of HD mating locus diversity through both time and space. These data have the potential to elucidate both the evolution of mating types in tetrapolar systems and how the effects of bottlenecking and invasion on the mating system in turn affect the distribution of genetic diversity throughout the population.
Evolution of heavy metal tolerance in a mycorrhizal fungus

WED 38

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Abstract

Fungi are ubiquitous in soil environments and are key players in soil systems processes, however little is known about how they deal with changes in their habitats. Genomic signatures of fungal adaptation can yield new insights on fungal evolution, as they should reflect the fungi’s unique mode of growth and lifestyle. We are using population genomics to investigate the genetic basis of heavy metal tolerance and environmental adaptation in Suillus luteus, a widespread symbiotic ectomycorrhizal fungus associated with pine trees. Available phenotypic data show that S. luteus isolates growing on heavy metal contaminated soils can tolerate high metal concentrations, while individuals from nearby non-contaminated sites show reduced growth and death when exposed to heavy metals. We hypothesize that heavy-metal tolerance in S. luteus is determined by few alleles with major effects on the ability to withstand high heavy metal concentrations. We sequenced whole genomes from a population (n=38) of Suillus luteus from a small geographical area in Belgium (~60 km radius) that included 3 severely metal-contaminated sites and 3 non-contaminated soils. Population genomic analyses show no evidence of population structure, suggesting ongoing gene flow. We aim to identify genomic signatures of selection and detect candidate genes underlying heavy metal adaptation. These regions likely contain genes encoding transmembrane transporters involved in metal homeostasis displaying copy number variation. Results from our study will elucidate on the evolutionary processes involved in environmental adaptation in fungi and set the stage for future studies testing the functional role of candidate genes.
Supergene convergent evolution in fungal mating-type chromosomes

WED 39

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Abstract

Convergent adaptation provides unique insights into the predictability of evolution and ultimately into processes of biological diversification.

Supergenes (beneficial gene linkage) are striking examples of adaptation, but little is known about their prevalence or evolution. A recent study on anther-smut fungi documented supergene formation by rearrangements linking two key mating-type loci, controlling pre- and post-mating compatibility. Here further high-quality genome assemblies reveal four additional independent cases of chromosomal rearrangements leading to regions of suppressed recombination linking mating-type loci in closely related species. Such convergent transitions in genomic architecture of mating-type determination indicate strong selection favoring linkage of mating-type loci into co-segregating supergenes. We find independent evolutionary strata (stepwise recombination suppression) in several species, with extensive rearrangements, gene losses, and transposable element accumulation. We thus show remarkable convergence in mating-type
chromosome evolution, recurrent supergene formation, and repeated
evolution of similar phenotypes through different genomic changes.
Reconstructing the core ectomycorrhizal community of *Populus trichocarpa*

**WED 40**

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**Abstract**

The ectomycorrhizal (ECM) fungi are mutualistic associates of some of the most dominant and speciose tree lineages on the planet, including pines, oaks, and eucalypts. Typically, any given ECM plant species will play host to hundreds of different ECM species, however, there are cases where a restricted community of ECM fungi can be found in specific ecological contexts such as with weakly ectotrophic hosts. *Populus trichocarpa*, or black cottonwood, has a diverse root microbiome dominated by endophytic members of Ascomycota. Like many salicaceous hosts, the ECM community of *P. trichocarpa* is restricted to a reduced core community with many of these species being host specific. Through a multi-year sampling effort and targeted meta-omics sequencing of the root microbiome, we have identified and isolated this core community in culture. It is now our objective to reassemble the core members of the ECM community with their native host to study ECM community assembly and function. This study focuses on an 8-member core community of both early and late successional species from distinct lineages across Ascomycota and Basidiomycota. We aim to test whether ECM community function reflects functional niche partitioning or whether members of a restricted ECM community are functionally redundant. Specifically, we are interested in species-specific contributions to the secreted metatranscriptome involved in nutrient decomplexing and acquisition from soil organic matter in relation to total nutrient flux with the plant host. This study also demonstrates novel methodology towards establishing an ECM community with a single plant host.
Evidence of multiple evolutionary origins of beetle-farmed decay fungi

WED 42

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Abstract

Ambrosia beetles are globally distributed wood borers that cultivate gardens of nutritional fungi to feed their young. They have organs, termed mycangia, to carry living fungal colonies while dispersing to new trees. The fungal symbionts of less than 5% of the more than 3,000 species of these beetles have been described and the ecologies of these fungi are largely unknown. Almost all known ambrosia fungi belong to Ascomycota and are not known to decay wood. It was recently shown that a globally-distributed clade of ambrosia beetles (Ambrosiodmus and Ambrosiophilus) farm a single species of aggressive wood-decaying polypore, Flavodon ambrosius. This symbiosis could affect wood-decay processes world-wide because these beetles are abundant where they are established and infest a diverse range of host trees. We examined fresh and preserved beetles of several genera from four continents using fungal culture work combined with high-throughput amplicon sequencing (HTS) using both Illumina and PacBio platforms. HTS allowed identification of multiple symbionts within the beetles. We incorporated single-copy fungal mock communities to parameterize our bioinformatics pipelines for both sequencing platforms. We discovered new diversity within the genus Flavodon from beetles from Asia and North America, including a new association with the beetle genus Beaverium. We also found evidence for multiple independent origins of new symbioses between the neotropical beetle genus Phloeoborus, and putative wood-decaying ambrosia fungi from two orders, Polyporales and Russulales. Our results demonstrate that symbioses between globally distributed ambrosia beetles and wood decay fungi are far more diverse and widespread than previously thought.
Touring with Trichomycetes: a magical time to master mycological mysteries in mosquitoes

WED 43

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Abstract

Trichomycetes are now recognized as an ecological group of microorganisms that include fungi and live in the digestive tracts of various arthropods. Though vast regions of the globe and huge numbers of this major animal group are vastly undersampled for these obligate endobionts, we have learned much about this symbiotic system with pulses of research spanning over 170 years. With the benefit of hindsight and an eye on what is available, in all respects, the willingness of an open mind and boldness to believe, or at least anticipate, predict and experiment, we can on occasion witness and/or participate in transformative shifts in our fundamental understanding of biology and evolution. The mystery of these microbes, in part owing to their microbial and endosymbiotic habit, is often elevated and enhanced when these mycological marvels are simply unmasked. Such is the backdrop for pondering the possibilities with trichomycete research on mosquitoes. Using examples from recent and ongoing field and lab-based studies using traditional morphological approaches combined with molecular tools and genomic probing highlights of recent advances are presented and suggested, with a sense of anticipation as much as answers. It is fair to say we still have much more to learn from the Trichomycetes and their long history as gut dwelling organisms, but we are doing so at a time when actual research pulses are being perceived and transformative shifts seem tangible and real. Of course, mosquitoes and other hosts, for so many reasons, are being intensively studied concurrently as well.
Signaling from below: rodents select for deeper fruiting truffles with stronger volatile emissions

WED 44

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Abstract

Truffles, the underground fruiting bodies of mycorrhizal fungi, have closely evolved with mammals for spore dispersal. Using four Elaphomyces truffle species we explored the role of fruiting depth, emissions of volatile organic compounds (VOC), and protein content in selection by five rodent species. Despite presumably easier access to the shallow fruiting truffle species, E. americanus and E. verruculosus (1.5 and 3.6 cm below the soil surface, respectively), most rodents selected for E. macrosporus and E. bartlettii that fruited deeper in the soil (5.9 and 8.6 cm, respectively). These deeper fruiting species had distinct VOC profiles and produced significantly higher quantities of odiferous compounds. However, Myodes gapperi (southern red-backed vole), a fungal specialist, selected for the truffles with high levels of digestible protein, E. verruculosus and E. macrosporus. Our results highlight the importance of chemical signals in truffle selection by rodents and suggest that VOCs are under strong selective pressures relative to protein rewards. For truffles, strong chemical signals likely allow detection by rodents deep within the soil where fruiting conditions are less influenced by drought or freezing. Strong chemical signals of truffles likely increase detection and reduce foraging effort by rodents, irrespective of fruiting depth. However, for species that depend on fungi as a major food source, protein content may be more important than fruiting depth and VOC emissions.
Survey of fungal pathogens in Pattoki, hub of nursery farming in Pakistan

WED 45

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Abstract

Pattoki is considered as the hub of the nursery farms in the Asian’s Subcontinent. It is known as “The City of Flowers” In nursery production here, the use of greenhouses with temperature regulation, selected growth substrate, irrigation and fertilization results in good seedling growth, but they may also favor the development of many biotic diseases especially fungal attack in rapidly growing seedlings. To contribute to the understanding of the origin of the disease, current project is designed to have answers of three questions: (1) what is the diversity of fungal pathogens in plant nurseries of Pattoki? (2) What is the specificity between the fungus, and the hosts plants? (3) are these pathogens invasive in this region, or native but overlooked? To survey these pathogenic species in their environment, infected leaves and stems are collected. Based on our first surveys, various species of \textit{Alternaria}, \textit{Cercospora}, \textit{Corynespora}, \textit{Cerotelium}, \textit{Leptosphaeria} are discovered causing leaf spot and rust on a wide range of economically important host plants. Here we present our preliminary morphological, cultural and molecular phylogenetic results and initial assessment of diseases scenario in nurseries of selected site. In Pakistan not significant projects have ever been designed to observe the fungal diseases in nurseries from taxonomic point of view. Thus this study on pathogens will be of utmost importance so that solutions can be found to eradicate as well as prevent their infection.
Engaging with the Dry Farming Collaborative to assess the efficacy of *Trichoderma harzianum* fungal endophytes to improve yield of diverse crops in water-limited farming systems

**WED 46**

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**Abstract**

Wild plants can adapt to extreme environments by maintaining symbiotic partnerships with certain fungal endophytes in a phenomenon known as habitat adapted symbiosis. Agricultural practitioners have begun applying particular strains of *Trichoderma harzianum* fungal endophytes, first isolated from wild, drought-tolerant grasses, to improve crop performance during periods of abiotic stress. We sought to test the efficacy of a commercial *T. harzianum* seed inoculant within the Dry Farming Collaborative, a group of farmers and researchers based in Oregon, USA, who are dedicated to innovation of dry farming practices, i.e., growing crops during the arid U.S. Pacific Northwest growing season without irrigation. During the summer of 2018 the Dry Farming Collaborative research participants tested whether the *T. harzianum* endophyte inoculant would increase yield in three varieties each of four dry farmed crops, maize (*Zea mays*), dry bean (*Phaseolus vulgaris*), winter squash (*Cucurbita maxima*), and tomato (*Solanum lycopersicum*), for a total of twelve drought-hardy varieties distributed across 14 sites in Oregon. The endophyte inoculant generally increased maize yield by 21% (p=0.045), and improved the yield of one of three bean varieties inoculated with the endophyte by 23% (p = 0.020). Squash and tomato yield were generally unaffected by the endophyte. Our results show endophyte inoculants such as *T. harzianum* have potential to stabilize yield in dry farmed systems, but their efficacy depends on their compatibility with crop genetics, site characteristics and their interactions with other members of the plant microbiome. Our ongoing research explores how microbe-microbe interactions may improve yield potential of this commercial endophyte.
Influence of host phylogeny and leaf chemistry on foliar endophytic communities of *Quercus*

**WED 47**

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**Abstract**

Every major lineage of land plants harbors highly diverse, horizontally transmitted endophytes that live within overtly healthy aboveground tissues such as leaves and stems. Both biotic and abiotic factors influence the diversity and community composition of endophytes, but the relative importance of these factors appears scale dependent. In local communities, host factors (i.e., leaf age, tissue type, genetics, or evolutionary history) often explains the greatest variation in endophyte community composition. Leaf chemistry and morphology also can influence endophyte dynamics, but often are confounded with host phylogeny such that the influence of leaf chemistry on endophyte assemblages is difficult to quantify. Here, we examined the impact of host phylogeny and leaf chemistry on the diversity and composition of foliar endophyte communities of oak (*Quercus* L., Fagaceae) in four distinct biogeographic areas of North America. Oaks constitute the dominant woody plant genus of North America and are distributed in a range of habitats from Canada to Mexico. Two major lineages of *Quercus* have diversified in parallel, such that distantly related species with convergent leaf traits often co-occur. We collected living, asymptomatic leaves of >20 oak species and measured total phenolic concentration from subsets of the same tissue sequenced using high-throughput next-generation sequencing (NGS) of ITS nrDNA. Using fungal phylogenetic- and biodiversity informatics tools, we will visualize the relationships of endophytic fungi to host phylogeny, leaf chemistry, and geography in an eco-evolutionary framework, and evaluate the factors shaping endophyte distributions in species of *Quercus* at local and continental scales.
Phylogenomics of ectomycorrhizal genera suggest that some may have a common, ancient origin in northern Gondwana

WED 48

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Abstract

Compared to boreal/temperate ecosystems, much less is known about ectomycorrhizal (EM) fungi in the tropics. This has hindered our ability to better understand the global biogeography of this fungal guild. For instance, it remains unknown whether tropical EM fungi have a common ancient origin in northern Gondwana, where contemporary, closely-related host trees exist. Therefore, through intensive examination of the EM fungi associated with Dicymbe and Gilbertiodendron—two closely related EM leguminous genera in the Neotropics and Afrotropics, respectively—we can expand our understanding of the origin and biogeography of this mutualism in the tropics. A matched, multi-year sporocarp sampling effort has occurred in both Dicymbe (Pakaraima Mountains, Guyana) and Gilbertiodendron (Dja Biosphere Reserve, Cameroon) monodominant forests. From both forest types we performed shotgun genome sequencing of Amanita, Cantharellus, and Clavulina species to obtain a large set of phylogenetic markers. Phylogenies using over 50 loci were constructed for each of the three genera, and molecular clock analyses were used to date the divergences of Dicymbe- and Gilbertiodendron-associated species. Our analyses suggest that Amanita evolved after the break-up of northern Gondwana, whereas the Cantharellus and Clavulina lineages appear to have evolved prior to the break-up of northern Gondwana. However, the analyses do not suggest a solely vicariant scenario for these latter two genera; dispersal has also likely played a role in driving their current cross-continental distribution.
Pyrophilous fungi: Widespread communities and novel life stages

WED 49

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Abstract

A review of pyrophilous or ‘fire loving’ fungal studies was conducted to predict the taxonomic composition of the fungal community expected to fruit after fire events. More than 500 species of Ascomycota and Basidiomycota have been reported in association with burned or heated areas and vegetation. Filtering for taxonomic synonyms and infrequently reported names reduces the number of pyrophilous taxa to about 100 species worldwide, 70% of which are Ascomycota (mostly Pezizales) and 30% Basidiomycota (mostly Agaricales). This exercise suggests endemism by continental scale is very low (about 25%), and that pyrophilous species are geographically widespread. However, there are very few reports of post-fire fungal communities from Africa, Asia, and South America, and detailed assessments of genetic diversity of most pyrophilous fungi remain to be made. About 70% of the pyrophilous fungal community is represented by ITS data on GenBank. Our presumption was that much of the pyrophilous community would be dominated by saprotrophic decomposers. However, many pyrophilous fungi match ITS sequences produced from cultures or environmental sequences of endophytic and endolichenic fungi. These results reinforce a suggestion made over 100 years ago by Fred Seaver, when he coined the term ‘pyrophilous fungi’, and hypothesized that burn fungi are present in pre-burn systems but evade detection.
New Zealand rust fungi: updates and recent additions

WED 50

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Abstract

Of the approximately 250 species of rust fungi (Pucciniales) recorded in New Zealand, about half are believed to be native or endemic since they occur on native plants. Work on a rust mycota of New Zealand has resulted in new collection localities of many species with a conservation status of data deficient. Molecular analyses have resulted in ten new combinations (\textit{comb. nov.}) and 11 new names (\textit{nom. nov.}). Although the number of non-native rusts has been rising steadily from 33 to over 120 in the last 150 years, the arrival in May 2017 of \textit{Austropuccinia psidii} (myrtle rust) is one of the most significant invasions to occur in New Zealand and is anticipated to have substantial biodiversity flow-on effects. \textit{Austropuccinia psidii} has a known host range of over 350 species in Myrtaceae and is already causing severe species declines in Australia where it has been since 2010. Unlike other non-native rust fungi, \textit{A. psidii} is primarily found on native species of Myrtaceae in NZ and three have been found to be highly susceptible. The number of susceptible hosts is expected to climb as \textit{A. psidii} has now been found in the native forest.
Multilocus phylogenies and morphological analyses revealed new and previously described *Ganoderma* species in South Africa

**WED 51**

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**Abstract**

*Ganoderma* is a cosmopolitan genus of Polypores that encompasses species important for forestry, medicine and cultural traditions. This study aimed at elucidating the identity and phylogenetic placements of a large collection of *Ganoderma* samples from South Africa. Identification was done based on phylogenetic analyses and morphological characters. Results from these analyses revealed that isolates from the collections belong to eight *Ganoderma* species. Of these *G. australe*, *G. austroafricanum*, *G. destructans* and *G. enigmaticum* have previously been reported from South Africa, while *G. cupreum* and *G. resinaceum* are new records for the country. The remaining two species are novel taxa belonging to subgen. *Elfvingia* and described as *G. acacicola* sp. nov. and *G. knysnamense* sp. nov. *Ganoderma acacicola* occurs on native and non-native hosts in four provinces of the country. The fungus is characterised by a perennial, triquetrous and broadly attached basidiome, a sulcate up to zonate yellowish brown to brown pilear surface, and ovoid to ellipsoid basidiospores. *Ganoderma knysnamense* was collected only in the Garden Route National Park where it was also the most abundant fungus among the species identified. It is distinguished by its applanate to ungulate, sometimes convex, and dimidiate to broadly attached basidiome, its chocolate-brown pilear surface covered with a hard woody-like crust and ellipsoid, broadly ellipsoid to ovoid basidiospores. In total, 15 *Ganoderma* species are now known from South Africa. The continual discovery of new species suggest that many more *Ganoderma* species are likely to be discovered in this country.
The MyCoPortal: Past, Present, and Future

WED 52

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Abstract

Digitization of fungal specimens began in earnest in 2012 with the funding of the Macrofungi Collections Consortium (MaCC) through NSF’s Advancing Digitization of Biological Collections program. In 2015 the Microfungi Collections Consortium (MiCC) was subsequently funded. The MaCC and MiCC projects digitized over 4.1M fungal specimens that are currently available online at the Mycology Collections Portal (http://mycoportal.org) and represent nearly all fungal specimens from the USA that have been deposited in fungaria in the last two centuries. These data allowed for a comprehensive survey of non-lichenized fungal specimens from North America (NA) that was recently published as a ‘protochecklist’. That publication documented roughly 45,000 NA taxa, of which nearly 20,000 names were supported by type specimens. While the work of compiling a more precise assessment of NA fungal biodiversity is just beginning, the MyCoPortal continues to support institutions in the USA and throughout the world in accessioning their mycological specimens. Recent developments include a GenBank sequence submission tool for ribosomal data, a Spatial Module with expanded mapping capabilities, improved data cleaning tools, an automated GBIF publisher, and the rMyCoPortal package for serving specimen data into the R environment. Future developments will include batch uploading of genetic data and links, a publication citations module, automated taxonomic thesaurus services via APIs, and a field guide that employs pattern recognition for automated identification. The MyCoPortal is now poised to facilitate and inform a wide variety of future studies focusing on fungal biodiversity, distributions, ecology, conservation, and phenology.
Teaching on fungal diversity in the tropics

WED 53

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Abstract

Fungi are a hyperdiverse group of organisms far from being adequately documented. Especially in the tropics, we are still in a pioneer phase concerning the scientific analysis of fungal species diversity. Meanwhile, most investigators working with fungi focus on model organisms or relatively small systematic groups, taxonomy often is considered old-fashioned, early career mycologists tend to focus on modern methods, and areas with natural vegetation are destroyed with numerous fungal species probably lost forever. This disturbing trend is addressed by a kaleidoscope of activities that aim at enhancing the attractiveness and valuation of fungal diversity in teaching and research; namely field forays, inventory projects, and checklist compilations, microscopic investigation of fresh fungal specimens, documentation of cellular structures by scientific drawings, attractive mycology lectures including information on the importance of fungi in various applied contexts, animated life cycles, life cycle puzzles, colourful textbook, diagrams for the illustration of ecosystem services of fungi, eLearning, and fungus exhibitions. By performing these activities, enthusiasm for fungal diversity shall be increased and young biologists may decide to become mycologists enthusiastic to contribute to the analysis of fungal diversity. For teaching material see: http://www.goethe-university-frankfurt.de/61705419/digitale-materialien
Morphology in the age of molecular techniques

WED 54

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Abstract

A majority of sequence data deposited in public databases are currently identified without the use of morphology. This is an increasing trend not only for environmental studies, but also in studies on diversity or systematics. Molecular tools offer a straightforward and reliable option for identification. Due to the emphasis on sequence barcoding and operational taxonomic unit (OTU) clustering, morphology is quickly being relegated to a formality of species description and rudimentary field identifications. Is there a place for morphology in this molecular age? Species description, a hallmark of biodiversity discovery and systematics, requires consistent selection of characters described, statistical support for morphometrics, precise use of terminology and interpretation of characters. The genus *Russula* has seen an increase in the number of species described, molecular support, and quality of descriptions during the past 12 years. Nevertheless, *Russula* descriptions show distinct inconsistencies between different regions and authors. We propose that morphology is an essential feature for identifying evolutionary and functional adaptations to ecological conditions. To illustrate this, we present instances of morphological adaptations in the genus *Russula* that have likely evolved in association with environmental and ecological shifts in the recent geological past. We also highlight five key morphological traits that are likely targets of local adaptation in mushroom-forming fungi. To support studies in evolution and functional traits of morphological characters, an emphasis on morphological standards is urgently needed.
Novel species-specific markers for the detection and identification of *Pseudonectria buxi* and *P. foliicola* from boxwood

**WED 55**

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**Abstract**

The ascomycete fungi *Pseudonectria buxi* and *P. foliicola* are the causal agents of Volutella stem and leaf blight, one of the most economically important diseases of boxwood worldwide. Traditional techniques for diagnosis of this disease are time-consuming, requiring days to weeks to provide results, complicating timely disease management decisions. The aim of this study is to develop a method of early detection and species-level identification of *Pseudonectria* affecting boxwood. Whole genome sequences of both *Pseudonectria* species and closely related, non-target fungi were generated using Illumina technology. Full protein datasets of target and non-target species were obtained either by using AUGUSTUS server predictions or recovered from public data repositories. Clusters of orthologous genes across the set of taxa were obtained using OrthoFinder. Gene clusters unique to the target taxa were used for primer design using PrimerBLAST. Candidate genes were screened in endpoint PCR assays with DNA from 40 curated representative isolates of *P. buxi* and *P. foliicola* and 20 non-target fungal species in the *Nectriaceae*. Three candidate protein coding genes (two targeting *P. buxi* and one targeting *P. foliicola*) were selected based on specificity and amplicon size. These candidate markers will be used in multiplex PCR assays using DNA extracted from affected or suspected plant samples applied to Whatman FTA cards. This study using whole genome datasets of plant pathogens demonstrates how this information can be used to discover new candidate markers for their rapid detection and identification, improving disease prevention, early detection and control strategies.
A genome atlas of the ectomycorrhizal genus *Suillus*: A model for fungus-plant mutualism belowground

WED 56

Nhu Nguyen¹, Lotus Lofgren², Anna Bazzicalupo³, Joske Ruytinx⁴, Hui-Ling Liao⁵, Ko-Hsuan Chen⁵, Amanda Certano², J. Alejandro Rojas⁶, Yi Hong Ke⁷, Looney Brian⁷, H. Van T. Cotter⁷, Jan Colpaert⁴, Alan Kuo⁸, Kerrie Barry⁸, Igor Grigoriev⁸, Thomas Bruns⁹, Sara Branco³, Peter Kennedy², Rytas Vilgalys⁷

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Abstract

The fungal genus *Suillus* represents one the most easily recognized mushrooms in forests worldwide. It has long been cited as a prime example of highly host-specific ectomycorrhizal fungal lineages, being associated almost exclusively with tree hosts in the family Pinaceae. Using a combination of ‘omics techniques, grounded in ecology and evolutionary biology, our project is generating a comprehensive and transdisciplinary understanding of *Suillus* species and their Pinaceae hosts. We have sequenced genomes that cover the breadth of all the major clades in the genus, as well as depth in a select number of species. Here we present an overview on the genomic features across the genus, a genome-level phylogeny to accurately infer the coevolutionary history of *Suillus* & Pinaceae hosts, determine the genomic signatures of host specificity, expand our understanding of the pangenome of *S. luteus* in native and introduced pine habitats, and dissect deeper into the evolution of heavy metal tolerance in *S. luteus*. Collectively, our project provides the first global-scale phylogenomic reconstruction of a keystone ectomycorrhizal genus, facilitates detailed knowledge about the evolutionary and ecological processes driving certain species in the genus, greatly advances our understanding of ectomycorrhizal fungal-host coevolution, and provides a powerful experimental model to understand fungal-plant mutualism.
Genetic diversity of endophytes influenced by host population structure and historical climate regimes

WED 57

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Abstract

Foliar fungal endophytes ubiquitously and asymptotically inhabit the photosynthetic tissues of all plant phyla but little is known about their population structure or the relative role of dispersal limitation and local adaptation in shaping their diversity. We intensively sampled diverse conifer communities throughout the northern hemisphere while focusing specifically on evergreen pine hosts and their host-specific endophyte, Lophodermium, with the goal of better understanding host-endophyte dynamics. We utilized a collection of cultures in conjunction with high-throughput sequencing to examine previously unexplored correlations between population structures of Lophodermium and multiple pine hosts. Our sampling in the Pacific Northwest in particular revealed two species of Lophodermium on the same pine hosts, but each had distinct population structure relative to the hosts, which may reveal how different population sizes, ecologies, or historical climate regimes influence current endophyte genetic diversity. Ongoing work will highlight the development of ddRAD sequencing to explore fine-scale genetic structures within several panmictic endophytes while exploring historical and current climate patterns as influential factors shaping their population structure. We present evidence for isolation by distance and cryptic speciation as important explanations for endophyte diversity.
Phylogenomic analyses of *Olpidium* reveal hard polytomies of the backbone of Kingdom Fungi

WED 58

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Abstract

*Olpidium* is a zoosporic fungal genus that includes obligate endoparasites of plants and nematodes. rDNA and multigene phylogenies suggest that accurate placement of *Olpidium* is pivotal to the understanding of flagellum loss in fungi, one of the key innovations in fungal evolution. We generated genome and transcriptome data from non-axenic *Olpidium* zoospores and removed contaminating sequences using metagenome methodology. We retrieved 295 protein markers from the cleaned *Olpidium* genome and from an additional 105 fungal genomes. We performed maximum likelihood phylogenetic reconstruction analyses using both super-alignment and super-tree approaches, as well as molecular dating analyses. Our results supported the placement of *Olpidium* with the non-flagellated fungi, although its exact position remained uncertain. We investigated the potential source of conflicting signals and tested the presence of hard polytomies along the backbone phylogeny of fungi. Our results detected little conflicting signal present among the sampled 295 genes, but did reveal two hard polytomies in early fungal evolution associated with the branching order of Blastocladiomycota and Chytridiomycota and the branching order of *Olpidium* and Zoopagomycota. Both polytomies were characterized by relatively short branch lengths and low phylogenetic conflict, a pattern consistent with even genome scale datasets possessing insufficient phylogenetic signal to resolve these nodes. Both nodes were associated with important morphological transitions, including the appearance of hyphal growth and the loss of flagellum. These morphological transitions enabled early fungi to explore new niches and resulted in rapid Precambrian diversifications of the ancestors of several phyla of fungi.
Lichen microbiomes: How much do we know and what’s next?

WED 59

Manuela Dal Forno\textsuperscript{1,2}, Eric Schuettpelez\textsuperscript{1}, Martin Grube\textsuperscript{3}

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Abstract

Over the past 15 years, molecular data have demonstrated that lichens are much more than simply a mycobiont and photobiont; they also include complex microbial communities, helping to form what we see in nature as the lichen thallus. Due to this added multiplicity and unique symbiotic structure, lichens have been described as mini-ecosystems, holobionts, or meta-organisms. While mycobionts and photobionts have been studied for over a century, we are just starting to tackle evolutionary questions related to lichen microbial diversity, which is composed primarily of bacteria and (other) fungi. Our current work aims to profile lichen core microbiomes (i.e., communities found across all samples within a grouping assigned a priori). We are investigating the taxonomic differences between these groupings, utilizing different high-throughput sequencing platforms and analysis pipelines. Our dataset includes hundreds of lichen samples from the Dictyonema clade (Hygrophoraceae, Agaricales), which is the most species-rich group of basidiolichens (136 currently accepted species in five genera) and sister to the non-lichenized monotypic fungal genus Eonema. Our results are providing key insight into which components are essential for lichen symbioses in Basidiomycota. We are also working to identify which bacteria are required to maintain functionality, stability, and survival of lichens.
Human mediated secondary contact between amphibian-killing chytrid strains produces an F2 hybrid

WED 60

Thomas Jenkinson1, Luis Felipe Toledo2, Kelly Zamudio3, Joyce Longcore4, Timothy James5, Erica Bree Rosenblum1

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Abstract

Global biodiversity is under threat from introductions of non-native fungal disease. The pathogenic chytrid, *Batrachochytrium dendrobatidis* (*Bd*), causes chytridiomycosis – the infectious disease implicated in frog, toad, and salamander population declines and extinctions worldwide. Where this fungus has been introduced, a single hypervirulent strain (*Bd*-GPL) proliferates through host populations. In the southern Atlantic Forest of Brazil, recent human introduction brought the globally invasive *Bd*-GPL strain into secondary contact with a distantly related, endemic strain, *Bd*-Brazil. In most anthropogenically mediated secondary contact scenarios such as this one, the epidemiological and evolutionary consequences of strain interaction remain unknown. We found that *Bd*, long considered obligately asexual, is capable of F2 hybridization following the human induced contact of divergent lineages. Using whole-genome sequencing of fungal isolates cultured from wild-infected Brazilian frogs, we characterize the hereditary relationships among disease populations in this strain invasion zone. Our analyses reveal regions of the *Bd* genome that are potentially driving ecological variation among invasive and endemic strains. The patterns of hybrid inheritance we observe offer new insights into the genetic underpinnings of fungal reproductive isolation, the process which ultimately results in speciation of emerging fungal diseases. These new southern Brazil hybrid strains we describe are of particular ecological and evolutionary concern because they demonstrate the ability of anthropogenic change to drive novel recombinant genetic variation in a deadly pathogen. These findings show how humans are actively creating new evolutionary trajectories for emerging diseases, such as chytridiomycosis, by creating novel mating opportunities between previously allopatric strains.
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